STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 115609

TO: Ralph J Gitomer **Location: Rem 3d65 / 3e71/** **Art Unit: 1651** **Thursday, March 11, 2004** **Case Serial Number: 10/043965**	**From: Noble Jarrell** **Location: Biotech-Chem Library** **Rem 1B71** **Phone: 272-2556** **Noble.jarrell@uspto.gov**

Search Notes

Ralph -

Noble conducted this search for you as a training exercise.
I supervised his work. If you have questions, please see me.

```
=> b reg
FILE 'REGISTRY' ENTERED AT 12:47:15 ON 11 MAR 2004
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
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Property values tagged with IC are from the ZIC/VINITI data file
provided by InfoChem.

STRUCTURE FILE UPDATES:   10 MAR 2004  HIGHEST RN 661450-61-9
DICTIONARY FILE UPDATES:  10 MAR 2004  HIGHEST RN 661450-61-9

TSCA INFORMATION NOW CURRENT THROUGH JANUARY 6, 2004

  Please note that search-term pricing does apply when
  conducting SmartSELECT searches.

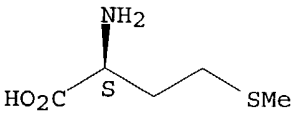
Crossover limits have been increased.  See HELP CROSSOVER for details.

Experimental and calculated property data are now available. For more
information enter HELP PROP at an arrow prompt in the file or refer
to the file summary sheet on the web at:
http://www.cas.org/ONLINE/DBSS/registryss.html


=> d ide l127 tot

L127 ANSWER 1 OF 8  REGISTRY  COPYRIGHT 2004 ACS on STN
RN   349086-43-7  REGISTRY
CN   L-Methionine-d3 (9CI)  (CA INDEX NAME)
FS   STEREOSEARCH
MF   C5 H8 D3 N O2 S
SR   CA
LC   STN Files:   CA, CAPLUS, USPATFULL
IL   3H-2

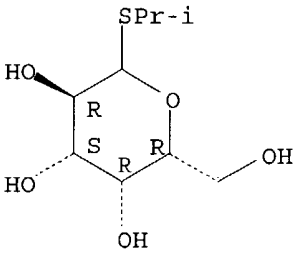
Absolute stereochemistry.
```




```
                3 REFERENCES IN FILE CA (1907 TO DATE)
                3 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L127 ANSWER 2 OF 8  REGISTRY  COPYRIGHT 2004 ACS on STN
RN   26112-89-0  REGISTRY
CN   D-Galactopyranoside, 1-methylethyl 1-thio- (9CI)  (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN   Galactopyranoside, isopropyl 1-thio-, D- (8CI)
OTHER NAMES:
CN   Isopropyl thiogalactoside
FS   STEREOSEARCH
MF   C9 H18 O5 S
LC   STN Files:   AGRICOLA, BEILSTEIN*, BIOBUSINESS, BIOSIS, BIOTECHNO, CA,
       CAPLUS, EMBASE, TOXCENTER, USPAT2, USPATFULL
         (*File contains numerically searchable property data)
```

Absolute stereochemistry.



PROPERTY DATA AVAILABLE IN THE 'PROP' FORMAT

25 REFERENCES IN FILE CA (1907 TO DATE)
25 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L127 ANSWER 3 OF 8 REGISTRY COPYRIGHT 2004 ACS on STN
RN **14762-74-4** REGISTRY
CN Carbon, isotope of mass 13 (8CI, 9CI) (CA INDEX NAME)
OTHER NAMES:
CN 13C
CN 13C
CN Carbon-13
CN Carbon-13 atom
CN Carbon-13C
DR 19709-48-9, 52453-99-3
MF C
CI COM
LC STN Files: AGRICOLA, ANABSTR, BIOBUSINESS, BIOSIS, BIOTECHNO, CA, CAPLUS, CASREACT, CBNB, CEN, CHEMCATS, CIN, CSCHEM, EMBASE, ENCOMPLIT, ENCOMPLIT2, ENCOMPPAT, ENCOMPPAT2, IFICDB, IFIPAT, IFIUDB, IPA, MSDS-OHS, NIOSHTIC, PIRA, PROMT, TOXCENTER, ULIDAT, USPAT2, USPATFULL, VTB

^{13}C

27168 REFERENCES IN FILE CA (1907 TO DATE)
102 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
27197 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L127 ANSWER 4 OF 8 REGISTRY COPYRIGHT 2004 ACS on STN
RN **14390-96-6** REGISTRY
CN Nitrogen, isotope of mass 15, at. (8CI, 9CI) (CA INDEX NAME)
OTHER NAMES:
CN 15N
CN Nitrogen-15
DR 93037-14-0
MF N
CI COM
LC STN Files: AGRICOLA, ANABSTR, BEILSTEIN*, BIOBUSINESS, BIOSIS, BIOTECHNO, CA, CAPLUS, CEN, CIN, EMBASE, IFICDB, IFIPAT, IFIUDB, IPA, PIRA, PROMT, TOXCENTER, USPAT2, USPATFULL, VTB
(*File contains numerically searchable property data)

^{15}N

7259 REFERENCES IN FILE CA (1907 TO DATE)
66 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
7272 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L127 ANSWER 5 OF 8 REGISTRY COPYRIGHT 2004 ACS on STN
RN **9002-07-7** REGISTRY
CN Trypsin (8CI, 9CI) (CA INDEX NAME)
OTHER NAMES:
CN Cocoonase
CN E.C. 3.4.21.4
CN E.C. 3.4.4.4
CN Parenzyme
CN Parenzymol
CN Pseudotrypsin
CN PTN
CN PTN 3.0 Special
CN PTN 3.0S
CN PTN 6.0S
CN PYN 3.0S
CN Sperm receptor hydrolase
CN Tripcellim
CN Trypsin V
CN Tryptar
CN Tryptec Formula 4X
CN Tryptec Formula One
CN Trypure
CN Typtar
DR 9068-82-0, 146990-35-4, 213972-07-7, 214265-38-0
MF Unspecified
CI COM, MAN
LC STN Files: ADISNEWS, AGRICOLA, ANABSTR, BIOBUSINESS, BIOSIS, BIOTECHNO, CA, CABA, CAPLUS, CASREACT, CBNB, CEN, CHEMCATS, CHEMINFORMRX, CHEMLIST, CIN, CSCHEM, DDFU, DIOGENES, DRUGU, EMBASE, HSDB*, IFICDB, IFIPAT, IFIUDB, IPA, MEDLINE, MRCK*, MSDS-OHS, NAPRALERT, NIOSHTIC, PIRA, PROMT, RTECS*, TOXCENTER, USPAT2, USPATFULL, VTB
(*File contains numerically searchable property data)
Other Sources: DSL**, EINECS**, TSCA**
(**Enter CHEMLIST File for up-to-date regulatory information)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

PROPERTY DATA AVAILABLE IN THE 'PROP' FORMAT

21595 REFERENCES IN FILE CA (1907 TO DATE)
781 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
21628 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L127 ANSWER 6 OF 8 REGISTRY COPYRIGHT 2004 ACS on STN
RN **9001-92-7** REGISTRY
CN Proteinase (9CI) (CA INDEX NAME)
OTHER NAMES:
CN α-N-Benzoyl-DL-arginine-p-nitroanilide hydrolase
CN 537 Acidic protease
CN Actinase
CN Alcalase 2.5LDX
CN Alkalase 2.4L FG
CN Alkalase 2.5L Type DX

CN Alkaline protease-L FG
CN ALP 901
CN Alphamalt BK 5020
CN Alphamalt LQ 4020
CN AO protease
CN APL 901
CN Aquatinase E
CN Arginine esterase
CN AS 1.398
CN AS 10
CN Azocaseinase
CN BAPAase
CN BAPNAase
CN Benzoyl arginine arylamidase
CN Benzoyl-DL-arginine-p-nitroanilide hydrolase
CN Bioprase SP 4FG
CN Bioprotease A
CN Bioprotease N 100P
CN Biopurase
CN Biosoft PW
CN Carbonyl hydrolase
CN Casein endopeptidase
CN Caseinase
CN Cleanase AP 100-PWC
CN Corolase 7089
CN Corolase L 10
CN DA 10
CN DA 10 (enzyme)
CN Denatyme AP
CN Deozyme
CN Durazyme 16.0L
CN Endopeptidase
CN Endopeptidase O
CN Endoprotease
CN Endoproteinase
CN Enzeco fungal acid protease
CN Enzylase K 40
CN Enzylon SAL
CN Enzylon SAL 300
CN Enzymes, proteolytic
CN Esteroproteinase
CN Everlase 16L
CN Everlase 16L Type EX
CN Everlase 8T
ADDITIONAL NAMES NOT AVAILABLE IN THIS FORMAT - Use FCN, FIDE, or ALL for DISPLAY
DR 9001-93-8, 9012-23-1, 9040-76-0, 125498-72-8, 125752-86-5, 123779-18-0, 124041-97-0, 120038-39-3, 120038-40-6, 105913-13-1, 118901-82-9, 144906-30-9, 143404-30-2, 143404-41-5, 80804-52-0, 116267-38-0, 117278-03-2, 117698-27-8, 118390-80-0
MF Unspecified
CI COM, MAN
LC STN Files: ADISNEWS, AGRICOLA, ANABSTR, BIOBUSINESS, BIOSIS, BIOTECHNO, CA, CAPLUS, CASREACT, CBNB, CEN, CHEMCATS, CHEMINFORMRX, CHEMLIST, CIN, CSCHEM, CSNB, DDFU, DIOGENES, DRUGU, EMBASE, IFICDB, IFIPAT, IFIUDB, IPA, MSDS-OHS, NAPRALERT, NIOSHTIC, PIRA, PLASPEC*, PROMT, RTECS*, TOXCENTER, TULSA, USPAT2, USPATFULL, VTB
(*File contains numerically searchable property data)
Other Sources: EINECS**, TSCA**
(**Enter CHEMLIST File for up-to-date regulatory information)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
39099 REFERENCES IN FILE CA (1907 TO DATE)
410 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
39153 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L127 ANSWER 7 OF 8 REGISTRY COPYRIGHT 2004 ACS on STN
RN **7782-39-0** REGISTRY
CN Deuterium (7CI, 8CI, 9CI) (CA INDEX NAME)
OTHER NAMES:
CN 2H
CN Deuterium (D2)
CN Deuterium mol.
CN Deuterium molecule
CN Dideuterium
CN Diplogen
CN Hydrogen, isotope of mass 2
CN Hydrogen-2
CN Hydrogen-d2
MF D2
CI COM
LC STN Files: ADISNEWS, AGRICOLA, ANABSTR, BEILSTEIN*, BIOBUSINESS, BIOSIS, BIOTECHNO, CA, CABA, CANCERLIT, CAOLD, CAPLUS, CASREACT, CBNB, CEN, CHEMCATS, CHEMINFORMRX, CHEMLIST, CHEMSAFE, CIN, CSCHEM, CSNB, DDFU, DETHERM*, DIPPR*, DRUGU, EMBASE, ENCOMPLIT, ENCOMPLIT2, ENCOMPPAT, ENCOMPPAT2, HSDB*, IFICDB, IFIPAT, IFIUDB, IPA, MEDLINE, MRCK*, MSDS-OHS, NIOSHTIC, PIRA, PROMT, SPECINFO, TOXCENTER, TULSA, USPAT2, USPATFULL, VTB
(*File contains numerically searchable property data)
Other Sources: DSL**, EINECS**, TSCA**
(**Enter CHEMLIST File for up-to-date regulatory information)

D—D

52778 REFERENCES IN FILE CA (1907 TO DATE)
277 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
52829 REFERENCES IN FILE CAPLUS (1907 TO DATE)
1 REFERENCES IN FILE CAOLD (PRIOR TO 1967)

L127 ANSWER 8 OF 8 REGISTRY COPYRIGHT 2004 ACS on STN
RN **4896-75-7** REGISTRY
CN Glycine-2,2-d2 (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)
OTHER NAMES:
CN 2,2-Dideuterioglycine
MF C2 H3 D2 N O2
CI COM
LC STN Files: BEILSTEIN*, CA, CAOLD, CAPLUS, CASREACT, CHEMCATS, CSCHEM, GMELIN*, USPATFULL
(*File contains numerically searchable property data)

$H_2N—CD_2—CO_2H$

65 REFERENCES IN FILE CA (1907 TO DATE)
66 REFERENCES IN FILE CAPLUS (1907 TO DATE)
14 REFERENCES IN FILE CAOLD (PRIOR TO 1967)

```
=> d his 4

     FILE 'HCAPLUS' ENTERED AT 12:46:34 ON 11 MAR 2004
L124           0 S 2002:539911:AN
L125           1 S 2002:539911/AN

     FILE 'REGISTRY' ENTERED AT 12:46:55 ON 11 MAR 2004

     FILE 'HCAPLUS' ENTERED AT 12:47:01 ON 11 MAR 2004
L126             TRA L125 1,1- RN :         8 TERMS

     FILE 'REGISTRY' ENTERED AT 12:47:01 ON 11 MAR 2004
L127           8 SEA L126

     FILE 'REGISTRY' ENTERED AT 12:47:15 ON 11 MAR 2004

=> b home
FILE 'HOME' ENTERED AT 12:47:50 ON 11 MAR 2004

=>
```

```
=> b hcap
FILE 'HCAPLUS' ENTERED AT 12:20:07 ON 11 MAR 2004
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
COPYRIGHT (C) 2004 AMERICAN CHEMICAL SOCIETY (ACS)
```



```
FILE COVERS 1907 - 11 Mar 2004  VOL 140 ISS 11
FILE LAST UPDATED: 10 Mar 2004  (20040310/ED)

 This file contains CAS Registry Numbers for easy and accurate
 substance identification.

'OBI' IS DEFAULT SEARCH FIELD FOR 'HCAPLUS' FILE

=> d all l122 hitstr tot
```

These papers include compounds mentioned in claims other than claim 1

```
L122 ANSWER 1 OF 5  HCAPLUS  COPYRIGHT 2004 ACS on STN
AN   2002:505014  HCAPLUS
DN   137:59881
ED   Entered STN:  05 Jul 2002
TI   Inverse labeling method for the rapid identification of
     marker/target proteins
IN   Wang, Yingqi Karen; Ma, Zhixiang; Quinn, Douglas Frederick; Fu, Emil W.
PA   Novartis A.-G., Switz.; Novartis-Erfindungen Verwaltungsgesellschaft
     m.b.H.
SO   PCT Int. Appl., 57 pp.
     CODEN: PIXXD2
DT   Patent
LA   English
IC   ICM  G01N033-68
CC   9-8 (Biochemical Methods)
FAN.CNT 1
     PATENT NO.        KIND  DATE           APPLICATION NO.  DATE
     ---------------   ----  --------       ---------------  --------
PI   WO 2002052271     A2    20020704       WO 2001-EP15228  20011221 <--
     WO 2002052271     A3    20021031
         W:  AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
             CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,
             HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LT, LU,
             LV, MA, MD, MK, MN, MX, NO, NZ, OM, PH, PL, PT, RO, RU, SE, SG,
             SI, SK, TJ, TM, TN, TR, TT, UA, US, UZ, VN, YU, ZA, ZW, AM, AZ,
             BY, KG, KZ, MD, RU, TJ, TM
         RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL,
             PT, SE, TR
     US 2002090652     A1    20020711       US 2001-16627    20011210 <--
     EP 1346229        A2    20030924       EP 2001-988064   20011221 <--
         R:  AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
             IE, SI, LT, LV, FI, RO, MK, CY, AL, TR
PRAI US 2000-257559P   P     20001222  <--
```

US 2001-332965P P 20011119
WO 2001-EP15228 W 20011221

AB A novel procedure for performing protein labeling for comparative proteomics termed inverse labeling is provided for the rapid identification of marker or target proteins. With this method, to evaluate protein expression of a disease or a drug treated sample in comparison with a control sample, two converse collaborative labeling expts. are performed in parallel. In one experiment the perturbed sample (by disease or by drug treatment) is isotopically heavy-labeled, whereas, the control is isotopically heavy-labeled in the second experiment When mixed and analyzed with its unlabeled or isotope light counterpart for differential comparison, a characteristic inverse labeling pattern is observed between the two parallel analyses for proteins that are differentially expressed to an appreciable level. In particularly useful embodiments, protein labeling is achieved through proteolytic 18O-incorporation into peptides as a result of proteolysis performed in 18O-water, metabolic incorporation of 15N (or 13C and 2H) into proteins, and chemical tagging proteins with an isotope-coded tag reagent such as an isotope-coded affinity tag reagent.

ST inverse labeling **marker** target **protein**; heavy isotope inverse labeling **protein**; oxygen 18 inverse labeling **protein**

IT Animal cell line
(CHO; inverse labeling method for rapid **identification** of **marker**/target **proteins**)

IT **Proteins**
RL: ANT (Analyte); BSU (Biological study, unclassified); RCT (Reactant); ANST (Analytical study); BIOL (Biological study); RACT (Reactant or reagent)
(HtrA; inverse labeling method for rapid **identification** of **marker**/target **proteins**)

IT **Time-of-flight mass spectrometry**
(**MALDI**; inverse labeling method for rapid **identification** of **marker**/target **proteins**)

IT Chromatography
(adsorption, **protein separation** by; inverse labeling method for rapid **identification** of **marker**/target **proteins**)

IT Precipitation (chemical)
(ammonium sulfate; inverse labeling method for rapid **identification** of **marker**/target **proteins**)

IT Algae
(anal. of cell lysates of; inverse labeling method for rapid **identification** of **marker**/target **proteins**)

IT **Proteins**
RL: ANT (Analyte); BSU (Biological study, unclassified); RCT (Reactant); ANST (Analytical study); BIOL (Biological study); RACT (Reactant or reagent)
(cell surface-associated; inverse labeling method for rapid **identification** of **marker**/target **proteins**)

IT Enzymes, uses
RL: CAT (Catalyst use); USES (Uses)
(cleaving labeled **proteins**; inverse labeling method for rapid **identification** of **marker**/target **proteins**)

IT Cytoplasm
(cytosol, **proteins** of; inverse labeling method for rapid **identification** of **marker**/target **proteins**)

IT Immunoassay
(immunopptn., **protein separation** by; inverse labeling method for rapid **identification** of **marker**/target **proteins**)

IT Animal tissue
Animal tissue culture
Body fluid
Cell
Databases
Development, mammalian postnatal
Disease, animal
Environment
Feces
Mass spectrometry
Nutrition, animal
Nutrition, microbial
Nutrition, plant
Physiology, animal
Protein degradation
Protein sequence analysis
Saliva
Tandem mass spectrometry
Tear (ocular fluid)
(inverse labeling method for rapid **identification** of **marker**/target **proteins**)

IT **Proteins**
RL: ANT (Analyte); BSU (Biological study, unclassified); RCT (Reactant); ANST (Analytical study); BIOL (Biological study); RACT (Reactant or reagent)
(inverse labeling method for rapid **identification** of **marker**/target **proteins**)

IT **Isotopes**
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); RCT (Reactant); ANST (Analytical study); BIOL (Biological study); RACT (Reactant or reagent); USES (Uses)
(inverse labeling method for rapid **identification** of **marker**/target **proteins**)

IT **Proteome**
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(inverse labeling method for rapid **identification** of **marker**/target **proteins**)

IT **Peptides**, biological studies
RL: BSU (Biological study, unclassified); RCT (Reactant); BIOL (Biological study); RACT (Reactant or reagent)
(inverse labeling method for rapid **identification** of **marker**/target **proteins**)

IT **Amino acids**, biological studies
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(inverse labeling method for rapid **identification** of **marker**/target **proteins**)

IT Reagents
RL: RCT (Reactant); RACT (Reactant or reagent)
(inverse labeling method for rapid **identification** of **marker**/target **proteins**)

IT **Proteins**
RL: ANT (Analyte); BSU (Biological study, unclassified); SPN (Synthetic preparation); ANST (Analytical study); BIOL (Biological study); PREP (Preparation)
(labeled; inverse labeling method for rapid **identification** of **marker**/target **proteins**)

IT Fluids
(lavage; inverse labeling method for rapid **identification** of **marker**/target **proteins**)

IT **Mass spectrometry**
(liquid chromatog. combined with; inverse labeling method for rapid **identification** of **marker**/target **proteins**)
IT **Protein** sequence analysis
(mass spectrometric; inverse labeling method for rapid **identification** of **marker**/target **proteins**)
IT Liquid chromatography
(mass spectrometry combined with; inverse labeling method for rapid **identification** of **marker**/target **proteins**)
IT **Proteins**
RL: ANT (Analyte); BSU (Biological study, unclassified); RCT (Reactant); ANST (Analytical study); BIOL (Biological study); RACT (Reactant or reagent)
(membrane; inverse labeling method for rapid **identification** of **marker**/target **proteins**)
IT **Laser ionization mass spectrometry**
(photodesorption, matrix-assisted, **TOF**; inverse labeling method for rapid **identification** of **marker**/target **proteins**)
IT **Laser desorption mass spectrometry**
(**photoionization, matrix-assisted, TOF**; inverse labeling method for rapid **identification** of **marker**/target **proteins**)
IT **Mass spectrometry**
(post source decay; inverse labeling method for rapid **identification** of **marker**/target **proteins**)
IT Affinity chromatography
Ion exchange chromatography
Isoelectric focusing
Reversed phase chromatography
Ultrafiltration
(**protein separation** by; inverse labeling method for rapid **identification** of **marker**/target **proteins**)
IT **Mass spectrometry**
(**protein** sequence anal.; inverse labeling method for rapid **identification** of **marker**/target **proteins**)
IT Chemicals
(**protein**-cleaving; inverse labeling method for rapid **identification** of **marker**/target **proteins**)
IT Organelle
(**proteins** of; inverse labeling method for rapid **identification** of **marker**/target **proteins**)
IT Biological materials
(reference; inverse labeling method for rapid **identification** of **marker**/target **proteins**)
IT Drugs
(sample treated with; inverse labeling method for rapid **identification** of **marker**/target **proteins**)
IT **Proteins**
RL: ANT (Analyte); PEP (Physical, engineering or chemical process); PYP (Physical process); ANST (Analytical study); PROC (Process)
(**separation**; inverse labeling method for rapid **identification** of **marker**/target **proteins**)
IT Chromatography
(size exclusion, **protein separation** by; inverse labeling method for rapid **identification** of **marker**/target **proteins**)
IT Affinity
(**tag** label; inverse labeling method for rapid

identification of **marker**/target **proteins**)
IT 79747-53-8, **Protein** Tyrosine Phosphatase
RL: ANT (Analyte); BSU (Biological study, unclassified); RCT (Reactant); ANST (Analytical study); BIOL (Biological study); RACT (Reactant or reagent)
(inverse labeling method for rapid **identification** of **marker**/target **proteins**)
IT 1333-74-0, Hydrogen, biological studies 7440-44-0, Carbon-12, biological studies 7727-37-9, Nitrogen-14, biological studies **7782-39-0**, Deuterium, biological studies 7782-44-7, Oxygen, biological studies **13965-97-4**, Sulfur-34, biological studies **13968-48-4**, Oxygen-17, biological studies **13981-57-2**, Sulfur-32, biological studies **14390-96-6**, 15N, biological studies **14762-74-4**, 13C, biological studies **14762-75-5**, Carbon-14, biological studies **14797-71-8**, Oxygen-18, biological studies
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); RCT (Reactant); ANST (Analytical study); BIOL (Biological study); RACT (Reactant or reagent); USES (Uses)
(inverse labeling method for rapid **identification** of **marker**/target **proteins**)
IT 50-99-7, D-Glucose, biological studies 14798-03-9D, Ammonium, salts
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(inverse labeling method for rapid **identification** of **marker**/target **proteins**)
IT **9002-07-7**, Trypsin
RL: CAT (Catalyst use); USES (Uses)
(inverse labeling method for rapid **identification** of **marker**/target **proteins**)
IT 7732-18-5, Water, reactions 14314-42-2, Water-18O
RL: RCT (Reactant); RACT (Reactant or reagent)
(inverse labeling method for rapid **identification** of **marker**/target **proteins**)
IT 7783-20-2, Ammonium sulfate, uses
RL: NUU (Other use, unclassified); USES (Uses)
(**protein separation** by precipitation with; inverse labeling method for rapid **identification** of **marker**/target **proteins**)
IT **7782-39-0**, Deuterium, biological studies **13965-97-4**, Sulfur-34, biological studies **13968-48-4**, Oxygen-17, biological studies **13981-57-2**, Sulfur-32, biological studies **14390-96-6**, 15N, biological studies **14762-74-4**, 13C, biological studies **14762-75-5**, Carbon-14, biological studies **14797-71-8**, Oxygen-18, biological studies
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); RCT (Reactant); ANST (Analytical study); BIOL (Biological study); RACT (Reactant or reagent); USES (Uses)
(inverse labeling method for rapid **identification** of **marker**/target **proteins**)
RN 7782-39-0 HCAPLUS
CN Deuterium (7CI, 8CI, 9CI) (CA INDEX NAME)

D—D

RN 13965-97-4 HCAPLUS
CN Sulfur, isotope of mass 34 (8CI, 9CI) (CA INDEX NAME)

^{34}S

RN 13968-48-4 HCAPLUS
CN Oxygen, isotope of mass 17, at. (8CI, 9CI) (CA INDEX NAME)

^{17}O

RN 13981-57-2 HCAPLUS
CN Sulfur, isotope of mass 32 (8CI, 9CI) (CA INDEX NAME)

^{32}S

RN 14390-96-6 HCAPLUS
CN Nitrogen, isotope of mass 15, at. (8CI, 9CI) (CA INDEX NAME)

^{15}N

RN 14762-74-4 HCAPLUS
CN Carbon, isotope of mass 13 (8CI, 9CI) (CA INDEX NAME)

^{13}C

RN 14762-75-5 HCAPLUS
CN Carbon, isotope of mass 14 (8CI, 9CI) (CA INDEX NAME)

^{14}C

RN 14797-71-8 HCAPLUS
CN Oxygen, isotope of mass 18, at. (8CI, 9CI) (CA INDEX NAME)

^{18}O

IT **9002-07-7**, Trypsin
RL: CAT (Catalyst use); USES (Uses)
(inverse labeling method for rapid **identification** of **marker**/target **proteins**)
RN 9002-07-7 HCAPLUS
CN Trypsin (8CI, 9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L122 ANSWER 2 OF 5 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 2002:450009 HCAPLUS
DN 137:17454
ED Entered STN: 14 Jun 2002
TI Isotope-coded ionization-enhancing reagents (ICIER) for high-throughput protein identification and quantitation using matrix-assisted laser

desorption ionization mass spectrometry
IN Qiu, Yongchang; Wang, Jack H.; Hewick, Rodney M.
PA Genetics Institute, LLC, USA
SO PCT Int. Appl., 45 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM G01N033-68
CC 9-16 (Biochemical Methods)
Section cross-reference(s): 6
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2002046770	A2	20020613	WO 2001-US50744	20011022 <--
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
AU 2002041732	A5	20020618	AU 2002-41732	20011022 <--
US 2003054570	A1	20030320	US 2001-44708	20011022 <--
PRAI US 2000-242645P	P	20001023 <--		
WO 2001-US50744	W	20011022		

AB The invention concerns arginine-containing cysteine-modifying compds. useful for MALDI-MS anal. of proteins are provided. These compds. termed isotope-coded ionization enhancement reagents (ICIER) can provide ionization enhancement in MALDI-MS, relative quantitation, and addnl. database searching constraints at the same time without any extra sample manipulation. More specifically, ICIER increase the ionization efficiency of cysteine-containing peptides by attachment of a guanidino functional group. ICIER also increase the overall hydrophilicity of these peptides due the hydrophilic nature of ICIER and thus increase the percentage of recovery of these peptides during sample handling and processing such as in-gel digestion or liquid chromatog. Finally, a combination of both light and heavy ICIER provides an accurate way to obtain relative quantitation of proteins by MALDI-MIS and addnl. database searching constraints (number of cysteine residues in every single peptide peak) to increase the confidence of protein identification by peptide mass mapping.

ST ionization reagent high throughput screening protein MALDI mass spectrometry
IT **Gel electrophoresis**
(PAGE; isotope-coded ionization-enhancing reagents (ICIER) for high-throughput protein identification and quantitation using matrix-assisted laser desorption ionization mass spectrometry)
IT **Peptides, analysis**
RL: ANT (Analyte); PRP (Properties); ANST (Analytical study)
(cysteine-containing; isotope-coded ionization-enhancing reagents (ICIER) for high-throughput protein identification and quantitation using matrix-assisted laser desorption ionization mass spectrometry)
IT Functional groups
(guanidino group; isotope-coded ionization-enhancing reagents (ICIER) for high-throughput protein identification and quantitation using matrix-assisted laser desorption ionization mass spectrometry)
IT Amide group
Amino group
Carboxyl group

Chemical chains
Digestion, chemical
Disulfide group
High throughput screening
Ionization
Labels
Mass spectrometry
Molecular association
Radiochemical analysis
Sample preparation
Sulfhydryl group
Test kits
(isotope-coded ionization-enhancing reagents (ICIER) for high-throughput protein identification and quantitation using matrix-assisted laser desorption ionization mass spectrometry)

IT **Peptides, analysis**
Proteins
RL: ANT (Analyte); ANST (Analytical study)
(isotope-coded ionization-enhancing reagents (ICIER) for high-throughput protein **identification** and quantitation using matrix-assisted laser desorption ionization mass spectrometry)

IT **Isotopes**
RL: ARG (Analytical reagent use); PRP (Properties); ANST (Analytical study); USES (Uses)
(isotope-coded ionization-enhancing reagents (ICIER) for high-throughput protein identification and quantitation using matrix-assisted laser desorption ionization mass spectrometry)

IT Reagents
RL: ARU (Analytical role, unclassified); ANST (Analytical study)
(isotope-coded ionization-enhancing reagents (ICIER) for high-throughput protein identification and quantitation using matrix-assisted laser desorption ionization mass spectrometry)

IT Functional groups
(maleimide; isotope-coded ionization-enhancing reagents (ICIER) for high-throughput protein identification and quantitation using matrix-assisted laser desorption ionization mass spectrometry)

IT **Laser ionization mass spectrometry**
(photodesorption, matrix-assisted; isotope-coded ionization-enhancing reagents (ICIER) for high-throughput protein identification and quantitation using matrix-assisted laser desorption ionization mass spectrometry)

IT **Laser desorption mass spectrometry**
(photoionization, matrix-assisted; isotope-coded ionization-enhancing reagents (ICIER) for high-throughput protein identification and quantitation using matrix-assisted laser desorption ionization mass spectrometry)

IT Functional groups
(α-haloacetyl; isotope-coded ionization-enhancing reagents (ICIER) for high-throughput protein identification and quantitation using matrix-assisted laser desorption ionization mass spectrometry)

IT **7782-39-0**, Deuterium, uses
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(isotope-coded ionization-enhancing reagents (ICIER) for high-throughput protein identification and quantitation using matrix-assisted laser desorption ionization mass spectrometry)

IT 434335-16-7P 434335-17-8P 434335-18-9P 434335-19-0P 434335-20-3P
RL: ARU (Analytical role, unclassified); SPN (Synthetic preparation); ANST (Analytical study); PREP (Preparation)
(isotope-coded ionization-enhancing reagents (ICIER) for high-throughput protein identification and quantitation using

matrix-assisted laser desorption ionization mass spectrometry)
IT **9001-92-7**, Proteinase
RL: NUU (Other use, unclassified); USES (Uses)
(isotope-coded ionization-enhancing reagents (ICIER) for high-throughput protein identification and quantitation using matrix-assisted laser desorption ionization mass spectrometry)
IT 52-90-4, Cysteine, properties
RL: PRP (Properties)
(isotope-coded ionization-enhancing reagents (ICIER) for high-throughput protein identification and quantitation using matrix-assisted laser desorption ionization mass spectrometry)
IT 161181-39-1 435313-81-8 435313-83-0 435313-85-2 435313-87-4
435313-89-6 435313-91-0 435313-93-2 435313-95-4 435313-97-6
435313-99-8 435314-01-5 435314-03-7 435314-05-9 435314-07-1
435314-09-3 435314-12-8 435314-14-0 435314-15-1 435314-16-2
435314-17-3 435314-18-4 435314-19-5 435314-25-3 435314-27-5
RL: PRP (Properties)
(unclaimed sequence; isotope-coded ionization-enhancing reagents (ICIER) for high-throughput protein identification and quantitation using matrix-assisted laser desorption ionization mass spectrometry)
IT **7782-39-0**, Deuterium, uses
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(isotope-coded ionization-enhancing reagents (ICIER) for high-throughput protein identification and quantitation using matrix-assisted laser desorption ionization mass spectrometry)
RN 7782-39-0 HCAPLUS
CN Deuterium (7CI, 8CI, 9CI) (CA INDEX NAME)

D—D

IT **9001-92-7**, Proteinase
RL: NUU (Other use, unclassified); USES (Uses)
(isotope-coded ionization-enhancing reagents (ICIER) for high-throughput protein identification and quantitation using matrix-assisted laser desorption ionization mass spectrometry)
RN 9001-92-7 HCAPLUS
CN Proteinase (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L122 ANSWER 3 OF 5 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:904715 HCAPLUS
DN 136:17697
ED Entered STN: 14 Dec 2001
TI Labeling of proteomic samples during proteolysis for quantitation and sample multiplexing
IN Figeys, Joseph Michel Daniel; Mann, Matthias; Stewart, Ian I.
PA MDS Proteomics, Inc., Can.
SO PCT Int. Appl., 68 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM G01N033-00
CC 9-5 (Biochemical Methods)
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2001094935	A2	20011213	WO 2001-IB1328	20010608 <--

WO 2001094935 A3 20021121
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
EP 1290450 A2 20030312 EP 2001-949829 20010608 <--
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR
US 2002076817 A1 20020620 US 2001-878750 20010611 <--
PRAI US 2000-210496P P 20000609 <--
US 2001-293664P P 20010525
WO 2001-IB1328 W 20010608

AB This invention relates to methods useful in the labeling of multiple polypeptide samples and subsequent anal. of these samples by mass spectrometry, particularly in the high throughput proteomic setting.

ST labeling proteome proteolysis quantitation multiplexing

IT Statistical mechanics
(deconvolution; labeling of proteomic samples during proteolysis for quantitation and sample multiplexing)

IT Amines, analysis
Halides
Phosphates, analysis
Thiols (organic), analysis
RL: ARU (Analytical role, unclassified); ANST (Analytical study)
(derivs.; labeling of proteomic samples during proteolysis for quantitation and sample multiplexing)

IT Affinity chromatography
Electrophoresis
Electrospray ionization mass spectrometry
Fast atom bombardment mass spectrometry
HPLC
Ion exchange chromatography
Isoelectric focusing
Protein degradation
Protein sequences
Simulation and Modeling, physicochemical
(labeling of proteomic samples during proteolysis for quantitation and sample multiplexing)

IT Albumins, analysis
Peptides, analysis
RL: ANT (Analyte); ANST (Analytical study)
(labeling of proteomic samples during proteolysis for quantitation and sample multiplexing)

IT **Laser ionization mass spectrometry**
(photodesorption, matrix-assisted; labeling of proteomic samples during proteolysis for quantitation and sample multiplexing)

IT **Laser desorption mass spectrometry**
(photoionization, matrix-assisted; labeling of proteomic samples during proteolysis for quantitation and sample multiplexing)

IT 7782-44-7, Oxygen, analysis **10028-17-8**, 3H, analysis
12586-59-3, Proton **14797-71-8**, 18O, analysis
RL: ARU (Analytical role, unclassified); ANST (Analytical study)
(labeling of proteomic samples during proteolysis for quantitation and sample multiplexing)

IT **9002-07-7**, Trypsin

RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(labeling of proteomic samples during proteolysis for quantitation and sample multiplexing)
IT **10028-17-8**, 3H, analysis **14797-71-8**, 18O, analysis
RL: ARU (Analytical role, unclassified); ANST (Analytical study)
(labeling of proteomic samples during proteolysis for quantitation and sample multiplexing)
RN 10028-17-8 HCAPLUS
CN Tritium (8CI, 9CI) (CA INDEX NAME)

T—T

RN 14797-71-8 HCAPLUS
CN Oxygen, isotope of mass 18, at. (8CI, 9CI) (CA INDEX NAME)

^{18}O

IT **9002-07-7**, Trypsin
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(labeling of proteomic samples during proteolysis for quantitation and sample multiplexing)
RN 9002-07-7 HCAPLUS
CN Trypsin (8CI, 9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L122 ANSWER 4 OF 5 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:790729 HCAPLUS
DN 133:331760
ED Entered STN: 10 Nov 2000
TI Method for the **comparative quantitative analysis** of **proteins** and other biological material by **isotopic labeling** and mass spectroscopy
IN Chait, Brian T.; Cowburn, David; Oda, Yoshi
PA The Rockefeller University, USA
SO PCT Int. Appl., 55 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM G01N033-00
ICS G01N024-00
CC 9-1 (Biochemical Methods)
Section cross-reference(s): 3
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000067017	A1	20001109	WO 2000-US12026	20000503 <--
	W: CA, JP				
	RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
	US 6391649	B1	20020521	US 1999-304799	19990504 <--
	US 2003077840	A1	20030424	US 2001-949510	20010906 <--
	US 6642059	B2	20031104		
PRAI	US 1999-304799	A	19990504 <--		

AB The present invention is a method for accurately comparing the levels of cellular components, such as proteins, present in samples which differ in some respect from each other using mass spectroscopy and isotopic labeling. A first sample of biol. matter, such as cells, is cultured in a first medium and a second sample of the same biol. matter is cultured in a second medium, wherein at least one isotope in the second medium has a different abundance than the abundance of the same isotope in the first medium. One of the samples is modulated, such as by treatment with a bacteria, a virus, a drug, hormone, a chemical or an environmental stimulus. The samples are combined and at least one protein is removed. The removed protein is subjected to mass spectroscopy to develop a mass spectrum. A ratio is computed between the peak intensities of at least one closely spaced pair of peaks to determine the relative abundance of the protein in each sample. The protein is identified by the mass spectrum or through other techniques known in the art. Modifications to the proteins, such as the phosphorylation of the protein, and the site of the modification may also be determined through the process of the present invention. The method is applicable to the components of any type of biol. matter which are ionizable and may therefore be analyzed by mass spectroscopy.

ST quant analysis **protein** biol **isotopic labeling** mass spectroscopy

IT Acylation
Glycosylation
(biol.; method for comparative quant. anal. of **proteins** and other biol. material by **isotopic labeling** and mass spectroscopy)

IT Affinity
Animal
Animal tissue
Animal tissue culture
Bacteria (Eubacteria)
Bioassay
Biological materials
Carcinogens
Cell
Chemicals
Chromatography
Culture media
Digestion, chemical
Drugs
Electrophoresis
Extraction
Feeding
Food
Gel electrophoresis
Gene therapy
Immunoassay
Isotope indicators
Mass spectra
Mass spectrometry
Metabolism, animal
Mixing
Organ, animal
Radiochemical analysis
Staining, biological
Ultracentrifugation
Virus
(method for comparative quant. anal. of **proteins** and other biol. material by **isotopic labeling** and mass spectroscopy)

IT Carbohydrates, analysis
Hormones, animal, analysis
Lipids, analysis
Nucleic acids
Proteins, general, analysis
RL: ANT (Analyte); ANST (Analytical study)
(method for comparative quant. anal. of **proteins** and other biol. material by **isotopic labeling** and mass spectroscopy)

IT **Peptides, analysis**
RL: ANT (Analyte); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study)
(method for comparative quant. anal. of **proteins** and other biol. material by **isotopic labeling** and **mass spectroscopy**)

IT Antibodies
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(method for comparative quant. anal. of **proteins** and other biol. material by **isotopic labeling** and mass spectroscopy)

IT Phosphorylation, biological
(**protein**; method for comparative quant. anal. of **proteins** and other biol. material by **isotopic labeling** and mass spectroscopy)

IT **Isotope indicators**
(stable; method for comparative quant. anal. of **proteins** and other biol. material by **isotopic labeling** and mass spectroscopy)

IT **Electrophoresis**
(two-dimensional; method for comparative quant. anal. of **proteins** and other biol. material by **isotopic labeling** and mass spectroscopy)

IT **7782-39-0**, Hydrogen 2, uses **13965-97-4**, Sulfur 34, uses **13968-48-4**, Oxygen-17, uses **14390-96-6**, Nitrogen-15, uses **14762-74-4**, Carbon-13, uses **14797-71-8**, Oxygen-18, uses
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(method for comparative quant. anal. of **proteins** and other biol. material by **isotopic labeling** and mass spectroscopy)

IT **9001-92-7**, Proteolytic enzyme **9002-07-7**, Trypsin
RL: CAT (Catalyst use); USES (Uses)
(method for comparative quant. anal. of **proteins** and other biol. material by **isotopic labeling** and mass spectroscopy)

RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE
(1) Gray; US 5572024 A 1996 HCAPLUS
(2) Kolhouse; US 5800979 A 1998 HCAPLUS

IT **7782-39-0**, Hydrogen 2, uses **13965-97-4**, Sulfur 34, uses **13968-48-4**, Oxygen-17, uses **14390-96-6**, Nitrogen-15, uses **14762-74-4**, Carbon-13, uses **14797-71-8**, Oxygen-18, uses
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(method for comparative quant. anal. of **proteins** and other biol. material by **isotopic labeling** and mass spectroscopy)

RN 7782-39-0 HCAPLUS
CN Deuterium (7CI, 8CI, 9CI) (CA INDEX NAME)

D—D

RN 13965-97-4 HCAPLUS
CN Sulfur, isotope of mass 34 (8CI, 9CI) (CA INDEX NAME)

^{34}S

RN 13968-48-4 HCAPLUS
CN Oxygen, isotope of mass 17, at. (8CI, 9CI) (CA INDEX NAME)

^{17}O

RN 14390-96-6 HCAPLUS
CN Nitrogen, isotope of mass 15, at. (8CI, 9CI) (CA INDEX NAME)

^{15}N

RN 14762-74-4 HCAPLUS
CN Carbon, isotope of mass 13 (8CI, 9CI) (CA INDEX NAME)

^{13}C

RN 14797-71-8 HCAPLUS
CN Oxygen, isotope of mass 18, at. (8CI, 9CI) (CA INDEX NAME)

^{18}O

IT **9001-92-7**, Proteolytic enzyme **9002-07-7**, Trypsin
RL: CAT (Catalyst use); USES (Uses)
(method for comparative quant. anal. of **proteins** and other biol. material by **isotopic labeling** and mass spectroscopy)
RN 9001-92-7 HCAPLUS
CN Proteinase (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 9002-07-7 HCAPLUS
CN Trypsin (8CI, 9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L122 ANSWER 5 OF 5 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:145059 HCAPLUS
DN 132:191408
ED Entered STN: 03 Mar 2000
TI Rapid quantitative analysis of proteins or protein function in complex mixtures using affinity labeling reagents and mass spectrometry
IN Aebersold, Rudolf Hans; Gelb, Michael H.; Gygi, Steven P.; Scott, C.

Ronald; Turecek, Frantisek; Gerber, Scott A.; Rist, Beate
PA University of Washington, USA
SO PCT Int. Appl., 116 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM C12Q001-00
ICS G01N033-573; G01N033-53; G01N033-567; G01N024-00
CC 9-5 (Biochemical Methods)
Section cross-reference(s): 6, 7, 26
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE	
PI	WO 2000011208	A1	20000302	WO 1999-US19415	19990825	<--
	W: AU, JP					
	RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE					
	AU 9956913	A1	20000314	AU 1999-56913	19990825	<--
	AU 755334	B2	20021212			
	EP 1105517	A1	20010613	EP 1999-943915	19990825	<--
	EP 1105517	B1	20031029			
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI					
	JP 2002523058	T2	20020730	JP 2000-566460	19990825	<--
	JP 3345401	B2	20021118			
	JP 2003107066	A2	20030409	JP 2002-208687	19990825	<--
	EP 1329513	A1	20030723	EP 2003-75828	19990825	<--
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI, CY					
	AT 253126	E	20031115	AT 1999-943915	19990825	<--
	US 6670194	B1	20031230	US 1999-383062	19990825	<--
	US 2002076739	A1	20020620	US 2001-839884	20010420	<--
	US 2003087322	A9	20030508			
PRAI	US 1998-97788P	P	19980825	<--		
	US 1998-99113P	P	19980903	<--		
	EP 1999-943915	A3	19990825	<--		
	JP 2000-566460	A3	19990825	<--		
	US 1999-383062	A3	19990825	<--		
	WO 1999-US19415	W	19990825	<--		

OS MARPAT 132:191408
AB Anal. reagents and mass spectrometry-based methods using these reagents for the rapid, and quant. anal. of proteins or protein function in mixts. of proteins are disclosed. The methods employ affinity labeled protein reactive reagents having three portions: an affinity label (A) covalently linked to a protein reactive group (PRG) through a linker group (L). The linker may be differentially isotopically labeled, e.g., by substitution of one or more atoms in the linker with a stable isotope thereof. These reagents allow for the selective isolation of peptide fragments or the products of reaction with a given protein (e.g., products of enzymic reaction) from complex mixts. The isolated peptide fragments or reaction products are characteristic of the presence of a protein or the presence of a protein function in those mixts. Isolated peptides or reaction products are characterized by mass spectrometric (MS) techniques. The reagents also provide for differential isotopic labeling of the isolated peptides or reaction products which facilitates quant. determination by mass spectrometry of the relative amount of proteins in different samples. The methods of this invention can be used for qual. and quant. anal. of global protein expression profiles in cells and tissues, to screen for and identify proteins whose expression level in cells, tissue or biol. fluids is affected by a stimulus or by a change in condition or cell state of the

cell, tissue or organism from which the sample originated. A conjugate of N-methylglycylbiotinamide acid and the Michael addition product of 4,7,10-trioxa-1,13-tridecanediamine and p-acrylamidophenyl-β-D-galactopyranoside was prepared for detecting β-D-galactosidase deficiency and GM1-gangliosidosis.

ST **protein** affinity labeling reagent mass spectrometry; **isotope labeling** reagent **protein** mass spectrometry; function **protein** analysis; enzyme substrate affinity **isotope label** reagent; biotin conjugate reagent galactosidase GM1 gangliosidosis

IT Glycols, biological studies
RL: ARG (Analytical reagent use); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(1,2-, conjugates with labeled protein-reactive reagents; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT Gangliosidosis
(GM1 gangliosidosis; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT Mucopolysaccharidosis
(Sanfilippo's syndrome, type B or D; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT Enzymes, analysis
RL: ANT (Analyte); BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(affinity labeling reagents containing substrates for; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT Amino group
Sulfhydryl group
(affinity labeling reagents reactive with, of proteins; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT Carboxylic acids, reactions
RL: RCT (Reactant); RACT (Reactant or reagent)
(affinity labeling reagents reactive with, of proteins; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT **Peptides, analysis**
RL: ANT (Analyte); FMU (Formation, unclassified); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); FORM (Formation, nonpreparative); USES (Uses)
(affinity-tagged, tagged proteins converted to; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and **mass spectrometry**)

IT Protein sequence analysis
(by tandem mass spectrometry; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT Haptens
RL: ARG (Analytical reagent use); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(conjugates, with labeled protein-reactive reagents; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT Tandem mass spectrometry
Tandem mass spectrometry

(electrospray-ionization; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT Congenital malformations
Lysosomal storage disease
(enzyme deficiency associated with; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT Fibroblast
(enzyme reagent response to, of patients with and without β-galactosidase deficiency; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT Disease, animal
(enzyme-deficiency; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT Avidins
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(immobilized, affinity column; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT Disulfide group
(linker containing, in labeling reagents; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT Mass spectrometry
Mass spectrometry
(liquid chromatog. combined with; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT Liquid chromatography
Liquid chromatography
(mass spectrometry combined with; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT Proteins, specific or class
RL: ANT (Analyte); ANST (Analytical study)
(membrane; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT Stress, animal
(phys., proteins expressed in response to; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT Saccharomyces cerevisiae
(protein expression in, with galactose or ethanol as carbon source; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT Isotopes
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(protein-reactive affinity reagent labeled with; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT Environment
Nutrition, animal
(proteins expressed in response to different conditions in; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT Chemicals
(proteins expressed in response to different; rapid quant. anal. of

proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT Organelle
(proteins of; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT Chromatography
Functional groups
Mass spectrometry
Tandem mass spectrometry
Test kits
(rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT Proteins, general, analysis
RL: AMX (Analytical matrix); ANT (Analyte); PRP (Properties); ANST (Analytical study)
(rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT Ovalbumin
RL: ANT (Analyte); RCT (Reactant); ANST (Analytical study); RACT (Reactant or reagent)
(rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT Reagents
RL: ARG (Analytical reagent use); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT Cell
(subcellular fractions of, proteins of; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT Electrospray ionization mass spectrometry
Electrospray ionization mass spectrometry
(tandem; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT Lactalbumins
RL: ANT (Analyte); RCT (Reactant); ANST (Analytical study); RACT (Reactant or reagent)
(α-; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT 9031-11-2, β-Galactosidase 9032-94-4 37288-40-7 37289-41-1, Heparin sulfamidase 60320-99-2, N-Acetylglucosamine-6-sulfatase
RL: ANT (Analyte); BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(affinity labeling reagents containing substrates for; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT 1192-20-7, Homoserine lactone
RL: RCT (Reactant); RACT (Reactant or reagent)
(affinity labeling reagents reactive with, of proteins; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT 221565-10-2P
RL: SPN (Synthetic preparation); PREP (Preparation)
(as GM1 internal standard; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT 259874-59-4P
RL: RCT (Reactant); SPN (Synthetic preparation); PREP (Preparation); RACT

(Reactant or reagent)
(as deuterated analog; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT 259874-28-7P 259874-29-8P
RL: RCT (Reactant); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); RACT (Reactant or reagent); USES (Uses)
(as enzyme substrate reagent; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT 221565-11-3P 259874-61-8P
RL: SPN (Synthetic preparation); PREP (Preparation)
(as internal standard; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT 259874-31-2 259874-32-3
RL: ARU (Analytical role, unclassified); ANST (Analytical study)
(as labeled internal standard; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT 221565-07-7P
RL: SPN (Synthetic preparation); PREP (Preparation)
(as reagent for diagnosing Sanfilippo syndrome type B; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT 259874-55-0P
RL: SPN (Synthetic preparation); PREP (Preparation)
(as reagent for diagnosing Sanfilippo syndrome type D; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT 252730-69-1 252730-69-1D, deuterium-labeled
RL: ARG (Analytical reagent use); RCT (Reactant); ANST (Analytical study); RACT (Reactant or reagent); USES (Uses)
(as reagent; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT 259874-30-1
RL: ANT (Analyte); FMU (Formation, unclassified); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); FORM (Formation, nonpreparative); USES (Uses)
(enzyme reagent cleavage to; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT 58-85-5 107-13-1, 2-Propenenitrile, reactions 111-46-6, reactions 407-25-0, Trifluoroacetic anhydride 769-39-1, 2,3,5,6-Tetrafluorophenol 13515-93-0, N-Methylglycine methyl ester hydrochloride 182267-11-4
RL: RCT (Reactant); RACT (Reactant or reagent)
(in preparation of reagent for diagnosing GM1-gangliosidosis; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT 22397-31-5P 24997-19-1P 53807-26-4P, 2-Propenenitrile-2,3,3-d3 112935-57-6P 142685-25-4P, 2,3,5,6-Tetrafluorophenyl trifluoroacetate 154024-76-7P 173341-32-7P 194920-70-2P 259874-33-4P 259874-35-6P 259874-36-7P 259874-38-9P 259874-39-0P 259874-40-3P
RL: RCT (Reactant); SPN (Synthetic preparation); PREP (Preparation); RACT (Reactant or reagent)
(in preparation of reagent for diagnosing GM1-gangliosidosis; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT 221565-06-6P 259874-34-5P 259874-37-8P

RL: SPN (Synthetic preparation); PREP (Preparation)
(in preparation of reagent for diagnosing GM1-gangliosidosis; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT 814-68-6, Acryloyl chloride
RL: RCT (Reactant); RACT (Reactant or reagent)
(in preparation of reagent for diagnosing Sanfilippo syndrome type B; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT 3386-87-6P 14419-59-1P 135253-87-1P 259874-41-4P 259874-42-5P 259874-43-6P 259874-47-0P
RL: RCT (Reactant); SPN (Synthetic preparation); PREP (Preparation); RACT (Reactant or reagent)
(in preparation of reagent for diagnosing Sanfilippo syndrome type B; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT 259874-45-8P
RL: SPN (Synthetic preparation); PREP (Preparation)
(in preparation of reagent for diagnosing Sanfilippo syndrome type B; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT 259874-51-6P 259874-53-8P
RL: RCT (Reactant); SPN (Synthetic preparation); PREP (Preparation); RACT (Reactant or reagent)
(in preparation of reagent for diagnosing Sanfilippo syndrome type D; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT 693-57-2 1670-26-4, Sphingosylphosphorylcholine 2238-90-6, Psychosine 2997-01-5 4246-51-9 259874-25-4 259874-26-5 259874-27-6
RL: RCT (Reactant); RACT (Reactant or reagent)
(in reagent preparation; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT 183896-00-6P 259874-63-0P 259874-66-3P 259874-74-3P
RL: RCT (Reactant); SPN (Synthetic preparation); PREP (Preparation); RACT (Reactant or reagent)
(in reagent preparation; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT 259874-68-5P 259874-70-9P 259874-76-5P
RL: SPN (Synthetic preparation); PREP (Preparation)
(in reagent preparation; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT 59-23-4, Galactose, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); PROC (Process); USES (Uses)
(protein expression in Saccharomyces cerevisiae grown in ethanol or; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT 50-99-7, Glucose, miscellaneous
RL: MSC (Miscellaneous)
(protein expression in Saccharomyces cerevisiae grown in galactose or ethanol instead of; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT 64-17-5, Ethanol, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); PROC (Process);

USES (Uses)
(protein expression in Saccharomyces cerevisiae grown in galactose or; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT 9001-50-7, Glyceraldehyde-3-phosphate dehydrogenase
RL: ANT (Analyte); RCT (Reactant); ANST (Analytical study); RACT (Reactant or reagent)
(rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT 9013-20-1D, Streptavidin, agarose-immobilized
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT 58-85-5D, Biotin, conjugates with labeled protein-reactive reagents
69-79-4D, Maltose, conjugates with labeled protein-reactive reagents
70-18-8D, Glutathione, conjugates with labeled protein-reactive reagents
71-00-1D, Histidine, oligo-, conjugates with labeled protein-reactive reagents, biological studies 139-13-9D, Nitrilotriacetic acid, conjugates with labeled protein-reactive reagents
RL: ARG (Analytical reagent use); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT **9001-92-7**, Proteolytic enzyme
RL: ARU (Analytical role, unclassified); CAT (Catalyst use); ANST (Analytical study); USES (Uses)
(rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT 259874-57-2
RL: MSC (Miscellaneous)
(rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

IT 9012-36-6, Agarose
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(streptavidin immobilized on; rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

RE.CNT 13 THERE ARE 13 CITED REFERENCES AVAILABLE FOR THIS RECORD

RE

(1) Adamczyk; US 5851781 A 1998 HCAPLUS
(2) Berninger; US 5880270 A 1999 HCAPLUS
(3) Dower; US 5958703 A 1999 HCAPLUS
(4) Ghazarossian; US 5614368 A 1997 HCAPLUS
(5) Griffiths; US 5965131 A 1999 HCAPLUS
(6) Kientsch-Engel; US 5863740 A 1999 HCAPLUS
(7) Magnani; US 5965457 A 1999 HCAPLUS
(8) Markert-Hahn; US 5514559 A 1996 HCAPLUS
(9) Schlieper; US 5658725 A 1997 HCAPLUS
(10) Shoseyov; US 5738984 A 1998 HCAPLUS
(11) Sigler; US 4798795 A 1989 HCAPLUS
(12) Tom-Moy; US 5527711 A 1996 HCAPLUS
(13) Vreeke; US 5534132 A 1996 HCAPLUS

IT **9001-92-7**, Proteolytic enzyme
RL: ARU (Analytical role, unclassified); CAT (Catalyst use); ANST (Analytical study); USES (Uses)
(rapid quant. anal. of proteins or protein function in complex mixts. using affinity labeling reagents and mass spectrometry)

RN 9001-92-7 HCAPLUS
CN Proteinase (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

=> d all hitstr l123 tot These citations include isotopes

L123 ANSWER 1 OF 15 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 2002:505323 HCAPLUS
DN 137:59910
ED Entered STN: 05 Jul 2002
TI Elemental analysis of tagged biologically active materials
IN Baranov, Vladimir; Tanner, Scott; Bandura, Dmitry; Quinn, Zoe
PA Mds Sciex, Can.
SO U.S. Pat. Appl. Publ., 20 pp.
CODEN: USXXCO
DT Patent
LA English
IC ICM G01N033-543
ICS B01D059-44
NCL 436518000
CC 9-16 (Biochemical Methods)
Section cross-reference(s): 1, 14
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 2002086441	A1	20020704	US 2001-905907	20010717 <--
	WO 2002054075	A1	20020711	WO 2001-CA1815	20011218 <--
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
	EP 1348127	A1	20031001	EP 2001-272578	20011218 <--
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				
PRAI	US 2000-258387P	P	20001228 <--		
	US 2001-905907	A1	20010717		
	WO 2001-CA1815	W	20011218		

AB Improved methods for the detection and quantitation of labeled biol. materials in a sample using elemental spectroscopic detection are described. Element-labeled biol. active materials, comprising antibodies, antigens, growth factors, hormones, receptors and other biol. active materials covalently attached to a stable elemental tag, can be used in specific binding assays and measured by elemental spectroscopic detection. Also described are methods for the determination of metals in samples of interest using specific antibodies to isolate the target metals and elemental spectroscopy for detection and quantitation.
ST elemental analysis tagged biol active
IT **Proteins**
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(A; elemental anal. of **tagged** biol. active materials)
IT Ions
(Atomic; elemental anal. of tagged biol. active materials)
IT Plasma
(Capacitively coupled; elemental anal. of tagged biol. active

materials)
IT Drugs
(Discovery; elemental anal. of tagged biol. active materials)
IT Immunoglobulins
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(G; elemental anal. of tagged biol. active materials)
IT Furnaces
(Graphite; elemental anal. of tagged biol. active materials)
IT Immunoassay
(Size Exclusion Gel Filtration; elemental anal. of tagged biol. active materials)
IT Bond
(covalent; elemental anal. of tagged biol. active materials)
IT Animal tissue
Animal tissue culture
Atomic mass
Biological materials
Cell
Chelation
Electric corona
Electrophoresis
Gels
Glow discharge
Human
Immunoassay
Inductively coupled plasma
Ions
Isotope indicators
Laser ablation
Mass spectrometry
Molecules
Samples
Separation
Spectrometers
Spectroscopy
Transformation, genetic
(elemental anal. of tagged biol. active materials)
IT Elements
Isotopes
Metals, analysis
Noble metals
Proteins
Rare earth metals, analysis
Transition metals, analysis
RL: ANT (Analyte); ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(elemental anal. of **tagged** biol. active materials)
IT Antibodies
Antigens
Growth factors, animal
Hormones, animal, uses
Nucleic acids
Receptors
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(elemental anal. of tagged biol. active materials)
IT Heart, disease
(infarction; elemental anal. of tagged biol. active materials)
IT Heart, disease
(ischemia; elemental anal. of tagged biol. active materials)
IT Brain, disease

Prion diseases
(mad cow; elemental anal. of tagged biol. active materials)
IT Plasma
(microwave induced; elemental anal. of tagged biol. active materials)
IT **Laser ionization mass spectrometry**
(photodesorption, matrix-assisted; elemental anal. of tagged biol. active materials)
IT **Laser desorption mass spectrometry**
(photoionization, matrix-assisted; elemental anal. of tagged biol. active materials)
IT **Gel electrophoresis**
(two-dimensional; elemental anal. of tagged biol. active materials)
IT 7439-88-5, Iridium, analysis 7440-05-3, Palladium, analysis 7440-06-4, Platinum, analysis 7440-16-6, Rhodium, analysis 7440-22-4, Silver, analysis 7440-57-5, Gold, analysis
RL: ANT (Analyte); ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(elemental anal. of tagged biol. active materials)
IT 9012-36-6, Agarose 14243-64-2, Nanogold 64134-30-1, Hexahistidine 125147-73-1, Dynabeads
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(elemental anal. of tagged biol. active materials)
IT 9003-05-8, Polyacrylamide
RL: PEP (Physical, engineering or chemical process); PYP (Physical process); PROC (Process)
(elemental anal. of tagged biol. active materials)

L123 ANSWER 2 OF 15 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 2002:276279 HCAPLUS
DN 136:291363
ED Entered STN: 12 Apr 2002
TI A method for the quantitative determination of one or more compounds
IN Bjellqvist, Bengt; Maloisel, Jean-Luc; Palmgren, Ronnie; Astrom, Jonas
PA Amersham Biosciences AB, Swed.
SO PCT Int. Appl., 44 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM G01N033-58
ICS G01N033-68
CC 9-16 (Biochemical Methods)
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2002029414	A2	20020411	WO 2001-EP11410	20011002 <--
	WO 2002029414	A3	20030130		
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
	AU 2002010519	A5	20020415	AU 2002-10519	20011002 <--
	EP 1325337	A2	20030709	EP 2001-978393	20011002 <--
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				
PRAI	SE 2000-3566	A	20001002 <--		

WO 2001-EP11410 W 20011002

AB The invention concerns a method for the quant. determination of the amount of one or more biomols., such as proteins or polypeptides, in one or more samples by utilizing sample unique tagging reagents. More specifically, the method comprises steps of providing at least two samples; reacting biomols. present in each sample with a sample unique mass tagging reagent to provide sample unique mass tagged forms thereof; combining tagged forms present in each sample to provide a single sample; co-separating, from the resulting sample, a mix of mass tagged forms of each of said biomols. into different fractions; subjecting, for each fraction, the mix to mass spectrometry to obtain a mass spectrum; and determining from signals in each mass spectrum, the amount of the biomol. corresponding to the spectrum in at least one of said samples relative to the amount of the same biomol. in at least one of the remaining samples. In an advantageous embodiment, the separation step is a gel electrophoresis step. In some cases, it may be advantageous to also include a step of digesting biomols., such as protein(s).

ST tag residue protein sepn digestion reagent chromatog mass spectrometry

IT Enzymes, uses
RL: NUU (Other use, unclassified); USES (Uses)
(digestion with; method for quant. determination of one or more compds.)

IT Biochemical molecules
Chromatography
Digestion, chemical
Electric charge
Electric field
Escherichia coli
Hydrophobicity
Isoelectric point
Mass spectrometry
Separation
Standards, purity and quality
(method for quant. determination of one or more compds.)

IT Nucleic acids
RL: ANT (Analyte); ANST (Analytical study)
(method for quant. determination of one or more compds.)

IT **Peptides, analysis**
Proteins
RL: ANT (Analyte); PRP (Properties); ANST (Analytical study)
(method for quant. determination of one or more compds.)

IT Elements
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(method for quant. determination of one or more compds.)

IT Reagents
RL: NUU (Other use, unclassified); USES (Uses)
(method for quant. determination of one or more compds.)

IT **Isotopes**
RL: PRP (Properties)
(method for quant. determination of one or more compds.)

IT Amines, properties
RL: PRP (Properties)
(primary; method for quant. determination of one or more compds.)

IT Albumins, analysis
RL: ANT (Analyte); ANST (Analytical study)
(serum; method for quant. determination of one or more compds.)

IT **Gel electrophoresis**
(two-dimensional; method for quant. determination of one or more compds.)

IT Lactoglobulins
RL: ANT (Analyte); ANST (Analytical study)

(β-; method for quant. determination of one or more compds.)
IT 1187-59-3, N-Methylacrylamide 2675-94-7, N,N-Diethylacrylamide
2680-03-7, N,N-Dimethylacrylamide 5883-17-0, N-Ethylacrylamide
25999-13-7, N-Propylacrylamide
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(method for quant. determination of one or more compds.)
IT 74225-65-3P 408305-10-2P
RL: ARG (Analytical reagent use); SPN (Synthetic preparation); ANST (Analytical study); PREP (Preparation); USES (Uses)
(method for quant. determination of one or more compds.)
IT 52-90-4, Cysteine, properties 58-61-7, Adenosine, properties 60-18-4, Tyrosine, properties
RL: PRP (Properties)
(protein residue; method for quant. determination of one or more compds.)

L123 ANSWER 3 OF 15 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 2002:276137 HCAPLUS
DN 136:305090
ED Entered STN: 12 Apr 2002
TI Whole cell engineering by mutagenizing a substantial portion of a starting genome and combining mutations with optional reiteration, identifying protein profiles by differential labeling and mass spectrometry, and by metabolic flux analysis
IN Short, Jay M.; Fu, Pengcheng; Latterich, Martin; Wei, Jing; Levin, Michael
PA Diversa Corporation, USA
SO PCT Int. Appl., 869 pp.
CODEN: PIXXD2
DT Patent
LA English
IC C12N015-00
CC 3-1 (Biochemical Genetics)
Section cross-reference(s): 9
FAN.CNT 40

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2002029032	A2	20020411	WO 2001-US31004	20011001 <--
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
AU 756201	B2	20030109	AU 2000-48933	20000731 <--
AU 2000048933	A5	20001005		
US 2002086279	A1	20020704	US 2001-875412	20010606 <--
US 6677115	B2	20040113		
WO 2001096551	A2	20011220	WO 2001-US19367	20010614 <--
WO 2001096551	A3	20020523		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
AU 2002011402	A5	20020415	AU 2002-11402	20011001 <--

PRAI US 2000-677584 A2 20000930 <--
US 2001-279702P P 20010328
WO 2001-US19367 W 20010614
AU 1997-11489 A3 19961206 <--
US 1997-988224 A1 19971210 <--
US 2000-594459 A2 20000614 <--
WO 2001-US31004 W 20011001

OS MARPAT 136:305090

AB An invention comprising cellular transformation, directed evolution, and screening methods for creating novel transgenic organisms having desirable properties. In one embodiment, this invention provides a method of generating a transgenic organism, such as a microbe or a plant, having a plurality of traits that are differentially activatable. This invention also provides a method of retooling genes and gene pathways by the introduction of regulatory sequences, such as promoters, that are operable in an intended host, this conferring operability to a novel gene pathway when it is introduced into an intended host. For example a novel man-made gene pathway, generated based on microbially-derived progenitor templates, that is operable in a plant cell. This invention also provides a method of generating novel host organisms having increased expression of desirable traits, recombinant genes, and gene products. This invention provides novel methods for determining polypeptide profiles, and protein expression variations, which methods are applicable to all sample types disclosed herein. The present invention provides methods of simultaneously identifying and quantifying individual proteins in complex protein mixts. by fragmentation, differential labeling, and tandem mass spectrometry. Addnl. this invention provides methods for cellular and metabolic engineering of new and modified phenotypes by using "online" or "real-time" metabolic flux anal.

ST whole cell engineering transformation directed evolution screening; genetic engineering whole cell directed evolution; bioengineering transformation directed evolution screening; protein differential labeling mass spectroscopy; metabolic flux analysis whole cell engineering

IT Engineering
(biochem.; whole cell engineering by mutagenizing a starting genome and combining mutations, identifying protein profiles by differential labeling and mass spectrometry, and by metabolic flux anal.)

IT Engineering
(bioengineering; whole cell engineering by mutagenizing a starting genome and combining mutations, identifying protein profiles by differential labeling and mass spectrometry, and by metabolic flux anal.)

IT **Peptides, analysis**
Proteins
RL: ANT (Analyte); ANST (Analytical study)
(differential labeling and holistic monitoring of; whole cell engineering by mutagenizing a starting genome and combining mutations, **identifying** protein profiles by differential labeling and mass spectrometry, and by metabolic flux anal.)

IT Functional groups
Linking agents
(differential labeling of peptides by; whole cell engineering by mutagenizing a starting genome and combining mutations, identifying protein profiles by differential labeling and mass spectrometry, and by metabolic flux anal.)

IT **Isotopes**
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(differential labeling of peptides by; whole cell engineering by mutagenizing a starting genome and combining mutations, identifying protein profiles by differential labeling and mass spectrometry, and by

metabolic flux anal.)
IT Biochemistry
(engineering; whole cell engineering by mutagenizing a starting genome and combining mutations, identifying protein profiles by differential labeling and mass spectrometry, and by metabolic flux anal.)
IT Immunoassay
(enzyme-linked immunosorbent assay, of proteins; whole cell engineering by mutagenizing a starting genome and combining mutations, identifying protein profiles by differential labeling and mass spectrometry, and by metabolic flux anal.)
IT Gene targeting
(gene knockin; whole cell engineering by mutagenizing a starting genome and combining mutations, identifying protein profiles by differential labeling and mass spectrometry, and by metabolic flux anal.)
IT Gene targeting
(gene knockout; whole cell engineering by mutagenizing a starting genome and combining mutations, identifying protein profiles by differential labeling and mass spectrometry, and by metabolic flux anal.)
IT Antibiotics
(holistic metaboic monitoring; whole cell engineering by mutagenizing a starting genome and combining mutations, identifying protein profiles by differential labeling and mass spectrometry, and by metabolic flux anal.)
IT Antibodies
Disaccharides
Lymphokines
Metals, analysis
Monosaccharides
Polysaccharides, analysis
Steroids, analysis
Toxins
RL: ANT (Analyte); ANST (Analytical study)
(holistic metaboic monitoring; whole cell engineering by mutagenizing a starting genome and combining mutations, identifying protein profiles by differential labeling and mass spectrometry, and by metabolic flux anal.)
IT Genome
(holistic monitoring; whole cell engineering by mutagenizing a starting genome and combining mutations, identifying protein profiles by differential labeling and mass spectrometry, and by metabolic flux anal.)
IT Carbohydrates, analysis
Glycoproteins
Lipids, analysis
Nucleic acids
Proteoglycans, analysis
Proteome
mRNA
RL: ANT (Analyte); ANST (Analytical study)
(holistic monitoring; whole cell engineering by mutagenizing a starting genome and combining mutations, identifying protein profiles by differential labeling and mass spectrometry, and by metabolic flux anal.)
IT Immunoassay
(immunoblotting, of proteins; whole cell engineering by mutagenizing a starting genome and combining mutations, identifying protein profiles by differential labeling and mass spectrometry, and by metabolic flux anal.)
IT Immunoassay

(immunopptn., of proteins; whole cell engineering by mutagenizing a starting genome and combining mutations, identifying protein profiles by differential labeling and mass spectrometry, and by metabolic flux anal.)

IT Functional groups
(isocyanato group, differential labeling of peptides by; whole cell engineering by mutagenizing a starting genome and combining mutations, identifying protein profiles by differential labeling and mass spectrometry, and by metabolic flux anal.)

IT Functional groups
(isothiocyanato group, differential labeling of peptides by; whole cell engineering by mutagenizing a starting genome and combining mutations, identifying protein profiles by differential labeling and mass spectrometry, and by metabolic flux anal.)

IT **Electrophoresis**
(of proteins; whole cell engineering by mutagenizing a starting genome and combining mutations, identifying protein profiles by differential labeling and mass spectrometry, and by metabolic flux anal.)

IT Acids, analysis
RL: ANT (Analyte); ANST (Analytical study)
(organic, holistic metaboic monitoring; whole cell engineering by mutagenizing a starting genome and combining mutations, identifying protein profiles by differential labeling and mass spectrometry, and by metabolic flux anal.)

IT Affinity chromatography
Chromatography
Fragmentation reaction
Liquid chromatography
Reversed phase HPLC
Size-exclusion chromatography
Tandem mass spectrometry
(protein; whole cell engineering by mutagenizing a starting genome and combining mutations, identifying protein profiles by differential labeling and mass spectrometry, and by metabolic flux anal.)

IT Immunoassay
(radioimmunoassay, of proteins; whole cell engineering by mutagenizing a starting genome and combining mutations, identifying protein profiles by differential labeling and mass spectrometry, and by metabolic flux anal.)

IT **Electrophoresis**
(two-dimensional, of proteins; whole cell engineering by mutagenizing a starting genome and combining mutations, identifying protein profiles by differential labeling and mass spectrometry, and by metabolic flux anal.)

IT Computer application
DNA microarray technology
Fluorescent dyes
Genetic engineering
Mass spectrometry
Metabolic pathways
Metabolism
Mutagenesis
Northern blot hybridization
Nucleic acid amplification (method)
Nucleic acid hybridization
Nucleic acid library
Transformation, genetic
(whole cell engineering by mutagenizing a starting genome and combining mutations, identifying protein profiles by differential labeling and mass spectrometry, and by metabolic flux anal.)

IT 58-85-5, Biotin 7440-44-0, Carbon-12, uses 7727-37-9, Nitrogen-14, uses **13965-97-4**, Sulfur-34, uses **13981-57-2**, Sulfur-32, uses **14390-96-6**, Nitrogen-15, uses **14762-74-4**, Carbon-13, uses **14798-12-0**, Boron-10, uses **14798-13-1**, Boron-11, uses
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(differential labeling of peptides by; whole cell engineering by mutagenizing a starting genome and combining mutations, identifying protein profiles by differential labeling and mass spectrometry, and by metabolic flux anal.)

IT 50-99-7, D-Glucose, analysis 56-81-5, Glycerol, analysis 57-50-1, Sucrose, analysis 64-19-7, Acetic acid, analysis 67-56-1, Methanol, analysis 107-92-6, Butyric acid, analysis 110-15-6, Succinic acid, analysis 328-42-7, Oxaloacetic acid 12408-02-5, Hydrogen ion, analysis
RL: ANT (Analyte); ANST (Analytical study)
(holistic metaboic monitoring; whole cell engineering by mutagenizing a starting genome and combining mutations, identifying protein profiles by differential labeling and mass spectrometry, and by metabolic flux anal.)

IT 409409-61-6 409409-62-7 409409-63-8 409409-64-9 409409-65-0, 1: PN: WO0229032 FIGURE: 6 unclaimed DNA 409409-66-1, 2: PN: WO0229032 FIGURE: 6 unclaimed DNA 409409-67-2, 3: PN: WO0229032 FIGURE: 6 unclaimed DNA 409409-68-3, 4: PN: WO0229032 FIGURE: 6 unclaimed DNA 409409-69-4, 5: PN: WO0229032 FIGURE: 6 unclaimed DNA 409409-70-7, 6: PN: WO0229032 FIGURE: 6 unclaimed DNA 409409-71-8, 7: PN: WO0229032 FIGURE: 6 unclaimed DNA 409409-72-9, 8: PN: WO0229032 FIGURE: 6 unclaimed DNA 409409-73-0, 9: PN: WO0229032 FIGURE: 7 unclaimed DNA 409409-74-1 409409-75-2
RL: PRP (Properties)
(unclaimed nucleotide sequence; whole cell engineering by mutagenizing a starting genome and combining mutations, identifying protein profiles by differential labeling and mass spectrometry, and by metabolic flux anal.)

IT **13965-97-4**, Sulfur-34, uses **13981-57-2**, Sulfur-32, uses **14390-96-6**, Nitrogen-15, uses **14762-74-4**, Carbon-13, uses **14798-12-0**, Boron-10, uses **14798-13-1**, Boron-11, uses
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(differential labeling of peptides by; whole cell engineering by mutagenizing a starting genome and combining mutations, identifying protein profiles by differential labeling and mass spectrometry, and by metabolic flux anal.)

RN 13965-97-4 HCAPLUS
CN Sulfur, isotope of mass 34 (8CI, 9CI) (CA INDEX NAME)

^{34}S

RN 13981-57-2 HCAPLUS
CN Sulfur, isotope of mass 32 (8CI, 9CI) (CA INDEX NAME)

^{32}S

RN 14390-96-6 HCAPLUS
CN Nitrogen, isotope of mass 15, at. (8CI, 9CI) (CA INDEX NAME)

^{15}N

RN 14762-74-4 HCAPLUS
CN Carbon, isotope of mass 13 (8CI, 9CI) (CA INDEX NAME)

^{13}C

RN 14798-12-0 HCAPLUS
CN Boron, isotope of mass 10 (8CI, 9CI) (CA INDEX NAME)

^{10}B

RN 14798-13-1 HCAPLUS
CN Boron, isotope of mass 11 (8CI, 9CI) (CA INDEX NAME)

^{11}B

L123 ANSWER 4 OF 15 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 2002:241288 HCAPLUS
DN 136:275646
ED Entered STN: 28 Mar 2002
TI Method and apparatus for detecting cancerous cells using molecules that change electrophoretic mobility
IN Allbritton, Nancy; Sims, Christopher
PA USA
SO U.S. Pat. Appl. Publ., 29 pp., Cont.-in-part of U.S. Ser. No. 358,504.
CODEN: USXXCO
DT Patent
LA English
IC ICM G01N033-574
NCL 435007230
CC 9-1 (Biochemical Methods)
Section cross-reference(s): 7, 14
FAN.CNT 6

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 2002037542	A1	20020328	US 2001-859650	20010517 <--
	US 6156576	A	20001205	US 1998-36706	19980306 <--
	US 6335201	B1	20020101	US 1999-358504	19990721 <--
	WO 2002092199	A1	20021121	WO 2002-US14755	20020509
	WO 2002092199	C1	20021227		
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
	EP 1392417	A1	20040303	EP 2002-769700	20020509
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,				

IE, SI, LT, LV, FI, RO, MK, CY, AL, TR

PRAI US 1998-36706 A2 19980306 <--
US 1999-358504 A2 19990721 <--
US 2001-859650 A 20010517
WO 2002-US14755 W 20020509

AB The activity of oncogenic intracellular chemical reactions of mols. is measured by the use of fluorescently labeled substrate mols. that undergo a change in electrophoretic mobility upon a chemical reaction such as that catalyzed by an enzyme or kinase. Specificity is achieved by using labeled substrate mols. that can be acted upon only by specific oncogenic enzymes. Thus the activity of an oncogenic enzyme or class of oncogenic enzymes can be determined Measurements are made with the intracellular presence of such substrate mols., at some time of interest. To ensure accuracy, measurements must be made in a timely manner so as to minimize chemical reactions occurring subsequent to the time of interest. Fast controllable laser lysis is used to obtain the contents of said cell or cells into which reporter substrate mols. have been introduced. The cell contents are then subjected to capillary electrophoresis and oncogenic enzymic activity is determined by comparing amts. of unaltered substrate mols. to the amts. of altered substrate mols. which are separated by the electrophoresis and identified by the presence of a fluorescent label.

ST app detecting cancer cell enzyme capillary electrophoresis; kinase cancer fluorescent substrate capillary electrophoresis

IT Animal cell line
(3T3; method and apparatus for detecting cancerous cells using mols. that change electrophoretic mobility)

IT **Capillary electrophoresis**
(PERT-CE (piezoelec. sampling/rapid translation/capillary electrophoresis); method and apparatus for detecting cancerous cells using mols. that change electrophoretic mobility)

IT Animal cell line
(RBL-2H3; method and apparatus for detecting cancerous cells using mols. that change electrophoretic mobility)

IT Fluorescent substances
(as label; method and apparatus for detecting cancerous cells using mols. that change electrophoretic mobility)

IT **Isotopes**
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(as labels; method and apparatus for detecting cancerous cells using mols. that change electrophoretic mobility)

IT Carbohydrates, reactions
Nucleic acids
Organic compounds, reactions
Peptides, reactions
Phospholipids, reactions
Polymers, reactions
Polysaccharides, reactions
Proteins
RL: ARG (Analytical reagent use); RCT (Reactant); ANST (Analytical study); RACT (Reactant or reagent); USES (Uses)
(as substrates; method and apparatus for detecting cancerous cells using mols. that change electrophoretic mobility)

IT Analytical apparatus
(biochem.; method and apparatus for detecting cancerous cells using mols. that change electrophoretic mobility)

IT Enzymes, analysis
RL: ANT (Analyte); CAT (Catalyst use); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(cancer-related; method and apparatus for detecting cancerous cells using mols. that change electrophoretic mobility)

IT Diagnosis
Diagnosis
(cancer; method and apparatus for detecting cancerous cells using mols. that change electrophoretic mobility)
IT Sampling apparatus
(cell; method and apparatus for detecting cancerous cells using mols. that change electrophoretic mobility)
IT Polymers, reactions
RL: ARG (Analytical reagent use); RCT (Reactant); ANST (Analytical study); RACT (Reactant or reagent); USES (Uses)
(conjugates, with fluorescent labels, as substrates; method and apparatus for detecting cancerous cells using mols. that change electrophoretic mobility)
IT **Peptides**, reactions
RL: ARG (Analytical reagent use); RCT (Reactant); ANST (Analytical study); RACT (Reactant or reagent); USES (Uses)
(conjugates, with fluorescent substances, as substrates; method and apparatus for detecting cancerous cells using mols. that change electrophoretic mobility)
IT Apparatus
(fast controlled cell lysis; method and apparatus for detecting cancerous cells using mols. that change electrophoretic mobility)
IT ESR (electron spin resonance)
(labels; method and apparatus for detecting cancerous cells using mols. that change electrophoretic mobility)
IT Analytical apparatus
Bioassay
Capillary electrophoresis
Capillary tubes
Computers
Cytolysis
Data processing
ESR spectroscopy
Electrophoresis
Electroporation
Fluorometry
Fusion, biological
Laser fluorometry
Mass spectrometry
Micellar electrokinetic capillary chromatography
Photomultipliers
Piezoelectric apparatus
Sensors
Voltammetry
(method and apparatus for detecting cancerous cells using mols. that change electrophoretic mobility)
IT Injectors
(microinjectors, in introducing substrate into cell; method and apparatus for detecting cancerous cells using mols. that change electrophoretic mobility)
IT Egg
(oocyte, Xenopus laevis; method and apparatus for detecting cancerous cells using mols. that change electrophoretic mobility)
IT Xenopus laevis
(oocytes; method and apparatus for detecting cancerous cells using mols. that change electrophoretic mobility)
IT Organelle
(pinosome, pinocytic loading, in introducing substrate into cell; method and apparatus for detecting cancerous cells using mols. that change electrophoretic mobility)

IT Phosphorylation, biological
(protein; method and apparatus for detecting cancerous cells using mols. that change electrophoretic mobility)
IT Liposomes
(vesicle fusion, in introducing substrate into cell; method and apparatus for detecting cancerous cells using mols. that change electrophoretic mobility)
IT Fusion, biological
(with vesicle, in introducing substrate into cell; method and apparatus for detecting cancerous cells using mols. that change electrophoretic mobility)
IT 405519-71-3P
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); PRP (Properties); RCT (Reactant); SPN (Synthetic preparation); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); RACT (Reactant or reagent); USES (Uses)
(as cdc2 kinase substrate; method and apparatus for detecting cancerous cells using mols. that change electrophoretic mobility)
IT 405095-29-6P
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); PRP (Properties); RCT (Reactant); SPN (Synthetic preparation); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); RACT (Reactant or reagent); USES (Uses)
(as substrate for PKA; method and apparatus for detecting cancerous cells using mols. that change electrophoretic mobility)
IT 405095-27-4P
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); PRP (Properties); RCT (Reactant); SPN (Synthetic preparation); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); RACT (Reactant or reagent); USES (Uses)
(as substrate; method and apparatus for detecting cancerous cells using mols. that change electrophoretic mobility)
IT 9002-98-6, PEI
RL: DEV (Device component use); USES (Uses)
(capillary coated with; method and apparatus for detecting cancerous cells using mols. that change electrophoretic mobility)
IT 142008-29-5, Protein kinase A 143375-65-9, Cdc2 kinase
RL: ANT (Analyte); BSU (Biological study, unclassified); CAT (Catalyst use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(method and apparatus for detecting cancerous cells using mols. that change electrophoretic mobility)
IT 141436-78-4, Protein kinase C
RL: ANT (Analyte); CAT (Catalyst use); ANST (Analytical study); USES (Uses)
(method and apparatus for detecting cancerous cells using mols. that change electrophoretic mobility)
IT 9031-44-1, Kinase 138238-67-2, Bcr-abl tyrosine kinase
RL: ANT (Analyte); CAT (Catalyst use); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(method and apparatus for detecting cancerous cells using mols. that change electrophoretic mobility)
IT 16561-29-8, PMA 30827-99-7, Pefabloc 65528-98-5 138067-56-8, Calcium Orange
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(method and apparatus for detecting cancerous cells using mols. that change electrophoretic mobility)
IT 136795-05-6DP, resin-bound
RL: PRP (Properties); RCT (Reactant); SPN (Synthetic preparation); PREP (Preparation); RACT (Reactant or reagent)

(method and apparatus for detecting cancerous cells using mols. that change electrophoretic mobility)
IT 405095-28-5P
RL: PRP (Properties); SPN (Synthetic preparation); PREP (Preparation)
(method and apparatus for detecting cancerous cells using mols. that change electrophoretic mobility)
IT 92557-80-7, 5-Carboxyfluorescein succinimidyl ester 117548-22-8
RL: RCT (Reactant); RACT (Reactant or reagent)
(method and apparatus for detecting cancerous cells using mols. that change electrophoretic mobility)
IT 121545-65-1 149155-45-3
RL: PRP (Properties)
(unclaimed sequence; method and apparatus for detecting cancerous cells using mols. that change electrophoretic mobility)

L123 ANSWER 5 OF 15 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 2002:107684 HCAPLUS
DN 136:145195
ED Entered STN: 10 Feb 2002
TI Cadherin-binding assay for identifying compounds which may protect stratified squamous epithelium against damage by noxious substances
IN Tobey, Nelia A.; Orlando, Roy C.
PA The Administrators of the Tulane Educational Fund, USA
SO PCT Int. Appl., 62 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM G01N033-68
CC 1-1 (Pharmacology)
Section cross-reference(s): 6, 13
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2002010767	A2	20020207	WO 2001-US23717	20010726 <--
WO 2002010767	A3	20030717		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

EP 1352247	A2	20031015	EP 2001-959274	20010726 <--

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR

PRAI US 2000-626196	A2	20000728 <--	
WO 2001-US23717	W	20010726	

AB The invention provides sequences of twenty five proteins and peptide fragments, which have sequence homol. with the extracellular domain of E-cadherin, including desmocollin 3, desmogleins, HA(V/N) domain of group 1 and 2 hemagglutinins from influenza strain A. Novel assay methods for screening compds. or identifying compds. useful for treating gastro-esophageal disease (GERD) are described, which involve determining the level of or presence of an interaction between the test compound and a polypeptide sequence comprising a portion of the extracellular domain of the junctional protein E-cadherin or a related polypeptide sequence.
ST cadherin binding protein homolog sequence human drug screening; squamous epithelium damage gastroesophageal reflux cadherin binding protein

IT Cadherins
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(E-; cadherin-binding assay for identifying compds. which may protect stratified squamous epithelium against damage by noxious substances)

IT **Gel electrophoresis**
(SDS, for determine protein fragmentation; cadherin-binding assay for identifying compds. which may protect stratified squamous epithelium against damage by noxious substances)

IT Plate glass
RL: DEV (Device component use); USES (Uses)
(as solid support for immobilizing cadherin and homologs; cadherin-binding assay for identifying compds. which may protect stratified squamous epithelium against damage by noxious substances)

IT Spheres
(beads, resin, as solid support for immobilizing cadherin and homologs; cadherin-binding assay for identifying compds. which may protect stratified squamous epithelium against damage by noxious substances)

IT Drug screening
Fluorescent indicators
Human
Influenza
Isotope indicators
Poisons, nonbiological source
Protein sequences
Rabbit
(cadherin-binding assay for identifying compds. which may protect stratified squamous epithelium against damage by noxious substances)

IT Gastric acid
RL: ADV (Adverse effect, including toxicity); BIOL (Biological study)
(cadherin-binding assay for identifying compds. which may protect stratified squamous epithelium against damage by noxious substances)

IT Hemagglutinins
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(cadherin-binding assay for identifying compds. which may protect stratified squamous epithelium against damage by noxious substances)

IT Cheek
Larynx
Pharynx
(damage, treatment of; cadherin-binding assay for identifying compds. which may protect stratified squamous epithelium against damage by noxious substances)

IT **Proteins**
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(desmocollin, 3; cadherin-binding assay for identifying compds. which may protect stratified squamous epithelium against damage by noxious substances)

IT Glycoproteins
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(desmoglein 1; cadherin-binding assay for identifying compds. which may protect stratified squamous epithelium against damage by noxious substances)

IT Glycoproteins

RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(desmoglein 3; cadherin-binding assay for identifying compds. which may protect stratified squamous epithelium against damage by noxious substances)

IT Glycoproteins
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(desmoglein, 2; cadherin-binding assay for identifying compds. which may protect stratified squamous epithelium against damage by noxious substances)

IT Mouth
(epithelium, damage, treatment of; cadherin-binding assay for identifying compds. which may protect stratified squamous epithelium against damage by noxious substances)

IT **Protein** motifs
(extracellular domain; cadherin-binding assay for identifying compds. which may protect stratified squamous epithelium against damage by noxious substances)

IT HPLC
Mass spectrometry
(for determine protein fragmentation; cadherin-binding assay for identifying compds. which may protect stratified squamous epithelium against damage by noxious substances)

IT Calorimetry
(for determine protein-binding complex stability; cadherin-binding assay for identifying compds. which may protect stratified squamous epithelium against damage by noxious substances)

IT Digestive tract, disease
(gastroesophageal reflux, treatment of; cadherin-binding assay for identifying compds. which may protect stratified squamous epithelium against damage by noxious substances)

IT Body fluid
(gastrointestinal fluid; cadherin-binding assay for identifying compds. which may protect stratified squamous epithelium against damage by noxious substances)

IT **Proteins**
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(immobilized, for cadherin-binding assay; cadherin-binding assay for identifying compds. which may protect stratified squamous epithelium against damage by noxious substances)

IT Antibodies
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(monoclonal; cadherin-binding assay for identifying compds. which may protect stratified squamous epithelium against damage by noxious substances)

IT Bioassay
(of amino acid, for determine protein fragmentation; cadherin-binding assay for identifying compds. which may protect stratified squamous epithelium against damage by noxious substances)

IT Titration
(of chemical or thermal denaturation, for determine protein-binding complex stability; cadherin-binding assay for identifying compds. which may protect stratified squamous epithelium against damage by noxious substances)

IT Esophagus
(permeability; cadherin-binding assay for identifying compds. which may protect stratified squamous epithelium against damage by noxious

substances)

IT Biological transport
(permeation, of esophagus; cadherin-binding assay for identifying compds. which may protect stratified squamous epithelium against damage by noxious substances)

IT Test tubes
(plastic or glass, as solid support for immobilizing cadherin and homologs; cadherin-binding assay for identifying compds. which may protect stratified squamous epithelium against damage by noxious substances)

IT Plates
(plastic, as solid support for immobilizing cadherin and homologs; cadherin-binding assay for identifying compds. which may protect stratified squamous epithelium against damage by noxious substances)

IT Sulfonic acids, biological studies
RL: PAC (Pharmacological activity); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(salts or esters; cadherin-binding assay for identifying compds. which may protect stratified squamous epithelium against damage by noxious substances)

IT Glass, uses
Plastics, uses
RL: DEV (Device component use); USES (Uses)
(slide or well, as solid support for immobilizing cadherin and homologs; cadherin-binding assay for identifying compds. which may protect stratified squamous epithelium against damage by noxious substances)

IT Epithelium
(squamous, stratified; cadherin-binding assay for identifying compds. which may protect stratified squamous epithelium against damage by noxious substances)

IT Electron density
(tracer; cadherin-binding assay for identifying compds. which may protect stratified squamous epithelium against damage by noxious substances)

IT Larynx
(vocal cord, damage, treatment of; cadherin-binding assay for identifying compds. which may protect stratified squamous epithelium against damage by noxious substances)

IT 395081-11-5 395081-13-7 395081-15-9 395081-16-0 395081-20-6 395170-80-6, E-cadherin (human) 395170-81-7, 155-261-E-cadherin (human) 395170-82-8, Desmoglein 1 (human) 395170-83-9, 52-157-Desmoglein 1 (human) 395170-84-0, Desmoglein 2 (human) 395170-85-1, 49-159-Desmoglein 2 (human) 395170-86-2, Desmoglein 3 (human) 395170-87-3, 52-157-Desmoglein 3 (human) 395170-88-4, Desmocollin 3 (human) 395170-89-5, 136-243-Desmocollin 3 (human) 395170-94-2 395170-95-3 395170-96-4 395170-97-5 395170-98-6 395170-99-7 395171-00-3 395171-01-4 395171-02-5 395171-03-6 395171-04-7 395171-05-8
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(amino acid sequence; cadherin-binding assay for identifying compds. which may protect stratified squamous epithelium against damage by noxious substances)

IT 9001-37-0, Glucose oxidase 9001-78-9, Alkaline phosphatase
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(as electron dense tracer; cadherin-binding assay for identifying compds. which may protect stratified squamous epithelium against damage by noxious substances)

IT 616-91-1, N-Acetylcysteine 7647-01-0, Hydrochloric acid, biological studies 9001-75-6, Pepsin
RL: ADV (Adverse effect, including toxicity); BIOL (Biological study)
(cadherin-binding assay for identifying compds. which may protect stratified squamous epithelium against damage by noxious substances)
IT 51023-76-8P, SITS 57680-56-5P, Sucrose octasulfate 389632-83-1P, CDDD 1192 389632-84-2P, CDDD 1193
RL: PAC (Pharmacological activity); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(cadherin-binding assay for identifying compds. which may protect stratified squamous epithelium against damage by noxious substances)
IT 7664-93-9D, Sulfuric acid, salts or esters
RL: PAC (Pharmacological activity); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(cadherin-binding assay for identifying compds. which may protect stratified squamous epithelium against damage by noxious substances)
IT 9003-99-0, Peroxidase
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(horseradish, as electron dense tracer; cadherin-binding assay for identifying compds. which may protect stratified squamous epithelium against damage by noxious substances)

L123 ANSWER 6 OF 15 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 2002:27082 HCAPLUS
DN 137:121820
ED Entered STN: 11 Jan 2002
TI Proteomics as a tool in biotechnology: facts and misconceptions
AU Rabilloud, Thierry
CS DBMS/BECP, CEA-Grenoble, Grenoble, F-38054, Fr.
SO American Biotechnology Laboratory (**2001**), 19(13), 10, 12
CODEN: ABLAEY; ISSN: 0749-3223
PB International Scientific Communications, Inc.
DT Journal
LA English
CC 9-16 (Biochemical Methods)
AB An evaluation of currently available techniques in proteomics is presented. These techniques include two-dimensional (2D) electrophoresis-mass spectrometry (MS), one-dimensional-electrophoresis-MS-MS and electrophoresis-free, liquid chromatog. (LC)-MS-MS. The 2D-electrophoresis technique is the only method that allows protein variants arising from different alleles or posttranslational modifications to be acquainted, provided these variations affect one of the separation criteria. However, this technique is insufficient for handling the complexity of proteomes. The 1D-electrophoresis is very efficient at yielding protein lists for small, not very complex samples such as Golgi preparation or nuclear pore. The idea underlying the electrophoresis-free technique is to analyze not proteins, which are large, complex and difficult objects, but only the peptides arising from the digestion of proteins. Since quantitation is a major issue in proteomics, strategies based on stable isotope labeling and enabling at least relative quantitation have been developed.
ST proteomics biotechnol electrophoresis
IT **Mass spectrometry**
(liquid chromatog. combined with; proteomics as a tool in biotechnol.)
IT Liquid chromatography
(mass spectrometry combined with; proteomics as a tool in biotechnol.)
IT Cell nucleus
(pore; proteomics as a tool in biotechnol.)
IT Alleles

Biotechnology
Digestion, chemical
Electrophoresis
Golgi apparatus
Isotope indicators
Mass spectrometry
Tandem mass spectrometry
(proteomics as a tool in biotechnol.)
IT **Peptides, analysis**
Proteins
Proteome
RL: ANT (Analyte); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study)
(proteomics as a tool in biotechnol.)
IT **Electrophoresis**
(two-dimensional; proteomics as a tool in biotechnol.)
RE.CNT 19 THERE ARE 19 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE
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L123 ANSWER 7 OF 15 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:693335 HCAPLUS
DN 135:223774
ED Entered STN: 21 Sep 2001
TI Mass labels for mass spectrometry
IN Schmidt, Gunter; Thompson, Andrew Hugin; Johnstone, Robert Alexander Walker
PA Brax Group Limited, UK
SO PCT Int. Appl., 102 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM C07H021-00
CC 9-5 (Biochemical Methods)
Section cross-reference(s): 73
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2001068664	A2	20010920	WO 2001-GB1122	20010314 <--
	WO 2001068664	A3	20020321		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,

CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR,
HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT,
LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU,
SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN,
YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,
DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF,
BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

EP 1275004 A2 20030115 EP 2001-911912 20010314 <--
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
IE, SI, LT, LV, FI, RO, MK, CY, AL, TR
JP 2003529059 T2 20030930 JP 2001-567754 20010314 <--
NO 2002004344 A 20021114 NO 2002-4344 20020912 <--
US 2003194717 A1 20031016 US 2003-221666 20030213 <--
PRAI GB 2000-6141 A 20000314 <--
WO 2001-GB1122 W 20010314
OS MARPAT 135:223774
AB Provided is a set of two or more mass labels, each label in the set comprising a mass marker moiety attached via a cleavable linker to a mass normalization moiety, the mass marker moiety being fragmentation resistant, wherein the aggregate mass of each label in the set may be the same or different and the mass of the mass marker moiety of each label in the set may be the same or different, and wherein in any group of labels within the set having a mass marker moiety of a common mass each label has an aggregate mass different from all other labels in that group, and wherein in any group of labels within the set having a common aggregate mass each label has a mass marker moiety having a mass different from that of all other mass marker moieties in that group, such that all of the mass labels in the set are distinguishable from each other by mass spectrometry.
ST mass spectrometry label
IT Amide group
(cleavable linker containing; mass labels for mass spectrometry)
IT Coupling agents
(cleavable, linking mass normalization group and mass marker; mass labels for mass spectrometry)
IT Gene
(expression, profiling; mass labels for mass spectrometry)
IT Collisions
(linker cleavable by; mass labels for mass spectrometry)
IT Amino group
Methyl group
Phenyl group
Phosphate group
(mass labels containing; mass labels for mass spectrometry)
IT Carbonates, uses
Halogen compounds
Isotopes
Phosphites
RL: ARG (Analytical reagent use); PRP (Properties); ANST (Analytical study); USES (Uses)
(mass labels containing; mass labels for mass spectrometry)
IT Affinity chromatography
Biochemical molecules
Capillary electrophoresis
Chromatography
DNA sequence analysis
Electrophoresis
Gel electrophoresis
HPLC

Mass
Mass spectrometry
Nucleic acid hybridization
Post-translational processing
Protein sequence analysis
Quadrupole mass spectrometry
Separation
cDNA sequences
(mass labels for mass spectrometry)

IT Glycoproteins, general, analysis
Peptides, analysis
Phosphoproteins
RL: ANT (Analyte); ANST (Analytical study)
(mass labels for mass spectrometry)

IT Amino acids, analysis
Nucleic acids
Proteins, general, analysis
RL: ANT (Analyte); ARG (Analytical reagent use); PRP (Properties); ANST (Analytical study); USES (Uses)
(mass labels for mass spectrometry)

IT cDNA
RL: ANT (Analyte); RCT (Reactant); ANST (Analytical study); RACT (Reactant or reagent)
(mass labels for mass spectrometry)

IT Primers (nucleic acid)
Probes (nucleic acid)
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(mass labels for mass spectrometry)

IT Antibodies
RL: ARG (Analytical reagent use); NUU (Other use, unclassified); ANST (Analytical study); USES (Uses)
(mass labels for mass spectrometry)

IT DNA
RL: ARG (Analytical reagent use); PRP (Properties); ANST (Analytical study); USES (Uses)
(mass labels for mass spectrometry)

IT Oligonucleotides
RL: ARG (Analytical reagent use); PRP (Properties); ANST (Analytical study); USES (Uses)
(mass labels for mass spectrometry)

IT RNA
RL: ARG (Analytical reagent use); PRP (Properties); ANST (Analytical study); USES (Uses)
(mass labels for mass spectrometry)

IT Reagents
RL: ARG (Analytical reagent use); PRP (Properties); ANST (Analytical study); USES (Uses)
(probes with different mass labels; mass labels for mass spectrometry)

IT Functional groups
(pyridinyl group, mass labels containing; mass labels for mass spectrometry)

IT Functional groups
(sulfate, mass labels containing; mass labels for mass spectrometry)

IT **Gel electrophoresis**
(two-dimensional; mass labels for mass spectrometry)

IT 21820-51-9, Phosphotyrosine
RL: ANT (Analyte); BPR (Biological process); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study); PROC (Process)
(antibody to; mass labels for mass spectrometry)

IT **7782-39-0**, Deuterium, uses **14762-74-4**, carbon-13, uses
14762-94-8, Fluorine atom, uses
RL: ARG (Analytical reagent use); PRP (Properties); ANST (Analytical study); USES (Uses)
(mass labels containing; mass labels for mass spectrometry)
IT 58-85-5, Biotin
RL: RCT (Reactant); RACT (Reactant or reagent)
(modified peptide reaction with; mass labels for mass spectrometry)
IT **7782-39-0**, Deuterium, uses **14762-74-4**, carbon-13, uses
RL: ARG (Analytical reagent use); PRP (Properties); ANST (Analytical study); USES (Uses)
(mass labels containing; mass labels for mass spectrometry)
RN 7782-39-0 HCAPLUS
CN Deuterium (7CI, 8CI, 9CI) (CA INDEX NAME)

D—D

RN 14762-74-4 HCAPLUS
CN Carbon, isotope of mass 13 (8CI, 9CI) (CA INDEX NAME)

^{13}C

L123 ANSWER 8 OF 15 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:669833 HCAPLUS
DN 135:269511
ED Entered STN: 13 Sep 2001
TI Evaluation of the efficiency of in-gel digestion of **proteins** by **peptide isotopic labeling** and MALDI mass spectrometry
AU Shevchenko, Anna; Shevchenko, Andrej
CS MPI of Molecular Cell Biology and Genetics, Dresden, 01307, Germany
SO Analytical Biochemistry (**2001**), 296(2), 279-283
CODEN: ANBCA2; ISSN: 0003-2697
PB Academic Press
DT Journal
LA English
CC 9-5 (Biochemical Methods)
AB A method for direct and quant. efficiency in-gel cleavage of proteins in order to outline a rational procedure for comparison of in gel digestion efficiency is described. The yield of digestion products was determined by MALDI MS using 18O-isotopically labeled peptides as internal stds. (c) 2001 Academic Press.
ST gel digestion protein peptide MALDI mass spectrometry
IT Albumins, analysis
Peptides, analysis
Proteins, general, analysis
RL: ANT (Analyte); ANST (Analytical study)
(in-gel digestion of **proteins** by **peptide isotopic labeling** and MALDI **mass spectrometry**)
IT Laser ionization mass spectrometry
(photodesorption, matrix-assisted; in-gel digestion of **proteins** by **peptide isotopic labeling** and MALDI mass spectrometry)
IT Laser desorption mass spectrometry

(photoionization, matrix-assisted; in-gel digestion of **proteins** by **peptide isotopic labeling** and MALDI mass spectrometry)

IT 288-32-4, Imidazole, uses 7440-22-4, Silver, uses 78642-64-5, Coomassie Blue
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(in-gel digestion of **proteins** by **peptide isotopic labeling** and MALDI mass spectrometry)

IT 14797-71-8, oxygen-18, analysis
RL: ARU (Analytical role, unclassified); ANST (Analytical study)
(in-gel digestion of **proteins** by **peptide isotopic labeling** and MALDI mass spectrometry)

RE.CNT 23 THERE ARE 23 CITED REFERENCES AVAILABLE FOR THIS RECORD

RE

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L123 ANSWER 9 OF 15 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:895432 HCAPLUS
DN 134:277441
ED Entered STN: 21 Dec 2000
TI Enhancing high-throughput proteome analysis: The impact of stable isotope labeling
AU Quadroni, Manfredo; James, Peter
CS Institute of Biochemistry, University of Lausanne, Epalinges, Switz.
SO Proteomics (**2001**), 151-169. Editor(s): Pennington, Stephen R.; Dunn, Michael J. Publisher: BIOS Scientific Publishers Ltd., Oxford, UK. CODEN: 69ATBR
DT Conference; General Review
LA English
CC 9-0 (Biochemical Methods)
Section cross-reference(s): 6
AB A review, with 68 refs., outlining the approaches and pitfalls in trying to automate protein identification and quantification methods for comprehensive proteome anal. Two-dimensional gel electrophoresis and mass spectrometry are given emphasis.

ST review proteome protein isotope labeling 2D electrophoresis mass spectrometry

IT **Mass spectrometry**
Process automation
(enhancing high-throughput proteome anal. and impact of stable isotope labeling)

IT **Proteins, general, analysis**
Proteome
RL: ANT (Analyte); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study)
(enhancing high-throughput proteome anal. and impact of stable isotope labeling)

IT **Isotopes**
RL: ARU (Analytical role, unclassified); ANST (Analytical study)
(enhancing high-throughput proteome anal. and impact of stable isotope labeling)

IT **Gel electrophoresis**
(two-dimensional; enhancing high-throughput proteome anal. and impact of stable isotope labeling)

RE.CNT 68 THERE ARE 68 CITED REFERENCES AVAILABLE FOR THIS RECORD

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L123 ANSWER 10 OF 15 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:858949 HCAPLUS
DN 134:112488
ED Entered STN: 08 Dec 2000
TI Enhanced TOF-SIMS imaging of a micropatterned protein by stable isotope protein labeling
AU Belu, Anna M.; Yang, Zhongping; Aslami, Ryan; Chilkoti, Ashutosh
CS Physical Electronics, Eden Prairie, MN, 55344, USA
SO Analytical Chemistry (**2001**), 73(2), 143-150
CODEN: ANCHAM; ISSN: 0003-2700
PB American Chemical Society
DT Journal
LA English
CC 9-5 (Biochemical Methods)
AB Patterning of biomols. on surfaces is an increasingly important technol. goal. Because the fabrication of biomol. arrays often involves stepwise, spatially resolved derivatization of surfaces, spectroscopic imaging of these arrays is important in their fabrication and optimization. Although imaging time-of-flight secondary ion mass spectrometry (TOF-SIMS) is a powerful method for spatially resolved surface anal., TOF-SIMS images of micropatterned proteins on organic substrates can be difficult to acquire, because of the lack of high intensity, protein-specific mol. ions that are essential for imaging under static conditions. In contrast, low-mass ions are of suitable intensity for imaging, but can originate from different chemical species on the surface. A potential solution to this problem is to utilize stable isotope labeled proteins, an approach that has heretofore not been explored in TOF-SIMS imaging of micropatterned proteins and peptides. To investigate the feasibility of stable isotope enhanced TOF-SIMS imaging of proteins, we synthesized 15N-labeled streptavidin by labeling of the protein during expression from a recombinant gene. The

spatial distribution of streptavidin bound to biotin micropatterns, fabricated on a polymer and on a self-assembled monolayer on gold, was imaged by TOF-SIMS. Imaging of high-intensity, low-m/z secondary ions (e.g., C15N-) unique to streptavidin enabled unambiguous spatial mapping of the micropatterned protein with a lateral resolution of a few micrometers. TOF-SIMS imaging of micropatterned 15N-labeled streptavidin also illustrated the exquisite sensitivity of TOF-SIMS to low fractional coverage of protein (5 Å effective thickness) in the background regions of the protein micropattern.

ST **protein** imaging TOF SIMS **isotope labeling**

IT **Proteins**, general, analysis
RL: ANT (Analyte); ANST (Analytical study)
(labeled with stable isotopes; **protein** micropattern imaging with TOF-SIMS by stable **isotope labeling**)

IT Electrospray ionization **mass spectrometry**
TOF-SIMS (time-of-flight secondary-ion mass spectrometry)
(**protein** micropattern imaging with **TOF**-SIMS by stable **isotope labeling**)

IT 58-85-5, Biotin
RL: ARU (Analytical role, unclassified); DEV (Device component use); ANST (Analytical study); USES (Uses)
(caged biotin self assembled monolayer; **protein** micropattern imaging with TOF-SIMS by stable **isotope labeling**)

IT **14390-96-6D**, 15N, **proteins** labeled with, analysis
RL: ANT (Analyte); ANST (Analytical study)
(**protein** micropattern imaging with TOF-SIMS by stable **isotope labeling**)

IT 9013-20-1D, Streptavidin, 15N labeled streptavidin
RL: ARU (Analytical role, unclassified); ANST (Analytical study)
(**protein** micropattern imaging with TOF-SIMS by stable **isotope labeling**)

RE.CNT 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD

RE

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(3) Kovacs, J; J Org Chem 1970, V35, P1810 HCAPLUS
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IT **14390-96-6D**, 15N, **proteins** labeled with, analysis
RL: ANT (Analyte); ANST (Analytical study)
(**protein** micropattern imaging with TOF-SIMS by stable **isotope labeling**)

RN 14390-96-6 HCAPLUS

CN Nitrogen, isotope of mass 15, at. (8CI, 9CI) (CA INDEX NAME)

^{15}N

L123 ANSWER 11 OF 15 HCAPLUS COPYRIGHT 2004 ACS on STN

AN 2000:756964 HCAPLUS

DN 133:319260

ED Entered STN: 27 Oct 2000

TI Polypeptide fingerprinting methods, metabolic profiling, apparatus, and bioinformatics database

IN Schneider, Luke V.; Hall, Michael P.; Petesch, Robert; Peterson, Jeffrey N.

PA Target Discovery, Inc., USA

SO PCT Int. Appl., 265 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM G01N027-26
ICS G01N027-447
CC 9-1 (Biochemical Methods)
Section cross-reference(s): 6, 13, 14
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2000063683	A1	20001026	WO 2000-US10504	20000419 <--
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
US 6379971	B1	20020430	US 2000-513395	20000225 <--
US 6537432	B1	20030325	US 2000-513486	20000225 <--
US 6677114	B1	20040113	US 2000-513907	20000225 <--
EP 1194768	A1	20020410	EP 2000-923511	20000419 <--
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 2003529044	T2	20030930	JP 2000-612736	20000419 <--
US 2002132357	A1	20020919	US 2002-68359	20020206 <--
US 2003119069	A1	20030626	US 2002-298268	20021115 <--
US 2003106797	A1	20030612	US 2003-341990	20030113 <--

PRAI US 1998-75715P	P	19980224	<--
US 1999-130238P	P	19990420	<--
US 2000-513395	A	20000225	<--
US 2000-513486	A	20000225	<--
US 2000-513907	A	20000225	<--
US 2000-551937	B1	20000419	<--
WO 2000-US10504	W	20000419	<--

AB The invention provides methods, compns., apparatus, and a computer data retrieval system for conducting proteomics and metabolic profiling on biol. samples. One apparatus comprises: a sample container (50); a plurality of separation capillaries (54, 64, 74); a plurality of fraction collection devices (60, 70); a detector (78); and an analyzer (82). Polypeptides are separated by multiple capillary electrophoresis devices and eluted polypeptides are analyzed by mass spectrometry.

ST polypeptide fingerprinting metab profiling bioinformatics database; capillary electrophoresis mass spectrometry app protein sepn analysis

IT **Capillary electrophoresis**
(2-dimensional; polypeptide fingerprinting methods and metabolic profiling and apparatus and bioinformatics database)

IT Myoglobins
RL: PRP (Properties); SPN (Synthetic preparation); PREP (Preparation)
(apo-, labeled with SPITC, inverted mass ladder sequencing of; polypeptide fingerprinting methods and metabolic profiling and apparatus and bioinformatics database)

IT **Capillary isoelectric focusing**
Capillary zone electrophoresis
Capillary zone electrophoresis
(apparatus; polypeptide fingerprinting methods and metabolic profiling and apparatus and bioinformatics database)

IT Amino acids, analysis
Carbohydrates, analysis
Fats and Glyceridic oils, analysis
Fatty acids, analysis
Nucleic acids
Nucleosides, analysis
Nucleotides, analysis
Polysaccharides, analysis
RL: ANT (Analyte); BOC (Biological occurrence); BSU (Biological study, unclassified); MFM (Metabolic formation); ANST (Analytical study); BIOL (Biological study); FORM (Formation, nonpreparative); OCCU (Occurrence)
(as metabolites; polypeptide fingerprinting methods and metabolic profiling and apparatus and bioinformatics database)

IT Metabolism, animal
(autism in relation to; polypeptide fingerprinting methods and metabolic profiling and apparatus and bioinformatics database)

IT Mental disorder
(autism, determination of role of metabolism in; polypeptide fingerprinting methods
and metabolic profiling and apparatus and bioinformatics database)

IT Samples
(biol.; polypeptide fingerprinting methods and metabolic profiling and apparatus and bioinformatics database)

IT **Gel electrophoresis**
Gel electrophoresis apparatus
(capillary; polypeptide fingerprinting methods and metabolic profiling and apparatus and bioinformatics database)

IT Escherichia coli
(detecting C-13 glucose metabolites in; polypeptide fingerprinting methods and metabolic profiling and apparatus and bioinformatics database)

IT **Time-of-flight mass spectrometry**
(electrospray, in inverted mass ladder sequencing of; polypeptide fingerprinting methods and metabolic profiling and apparatus and bioinformatics database)

IT Fluorescent substances
(fluorophores, for detection enhancement; polypeptide fingerprinting methods and metabolic profiling and apparatus and bioinformatics database)

IT Containers
(for samples; polypeptide fingerprinting methods and metabolic profiling and apparatus and bioinformatics database)

IT **Capillary electrophoresis**
(gel; polypeptide fingerprinting methods and metabolic profiling and apparatus and bioinformatics database)

IT Stress, animal
Stress, microbial
Stress, plant
(gene expression in relation to; polypeptide fingerprinting methods and metabolic profiling and apparatus and bioinformatics database)

IT Conalbumins
RL: ANT (Analyte); PEP (Physical, engineering or chemical process); RCT (Reactant); ANST (Analytical study); PROC (Process); RACT (Reactant or reagent)
(hen egg white, separation of mixture containing; polypeptide fingerprinting methods and metabolic profiling and apparatus and bioinformatics database)

IT **Isotopes**
RL: ARG (Analytical reagent use); BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); RCT (Reactant); ANST (Analytical study); BIOL (Biological study); PROC (Process); RACT (Reactant or reagent); USES (Uses)
(in analyzing metabolic pathways; polypeptide fingerprinting methods

and metabolic profiling and apparatus and bioinformatics database)

IT **Proteins, specific or class**
RL: ANT (Analyte); PRP (Properties); ANST (Analytical study)
(labeled; polypeptide fingerprinting methods and metabolic profiling and apparatus and bioinformatics database)

IT **Protein** sequence analysis
Protein sequence analysis
(mass spectrometric; polypeptide fingerprinting methods and metabolic profiling and apparatus and bioinformatics database)

IT Neoplasm
(metastasis; polypeptide fingerprinting methods and metabolic profiling and apparatus and bioinformatics database)

IT **Mass spectrometry**
(neg.-ion; polypeptide fingerprinting methods and metabolic profiling and apparatus and bioinformatics database)

IT Acids, analysis
RL: ANT (Analyte); BOC (Biological occurrence); BSU (Biological study, unclassified); MFM (Metabolic formation); ANST (Analytical study); BIOL (Biological study); FORM (Formation, nonpreparative); OCCU (Occurrence)
(organic, as metabolites; polypeptide fingerprinting methods and metabolic profiling and apparatus and bioinformatics database)

IT Analytical apparatus
Apparatus
Bioinformatics
Biological materials
Capillary electrophoresis
Capillary electrophoresis apparatus
Capillary isoelectric focusing
Capillary zone electrophoresis
Collecting apparatus
Computer program
Computers
Databases
Diagnosis
Mass spectrometers
Mass spectrometry
Metabolic pathways
Metabolism
Neoplasm
Protein sequences
Sample preparation
Sensors
(polypeptide fingerprinting methods and metabolic profiling and apparatus and bioinformatics database)

IT **Peptides, analysis**
Proteins, general, analysis
RL: ANT (Analyte); BOC (Biological occurrence); BSU (Biological study, unclassified); MFM (Metabolic formation); PRP (Properties); ANST (Analytical study); BIOL (Biological study); FORM (Formation, nonpreparative); OCCU (Occurrence)
(polypeptide fingerprinting methods and metabolic profiling and apparatus and bioinformatics database)

IT Animal tissue
Cell
Pathology
(protein expression fingerprint for; polypeptide fingerprinting methods and metabolic profiling and apparatus and bioinformatics database)

IT **Mass spectrometry**
Mass spectrometry
(protein sequence anal.; polypeptide fingerprinting methods and

metabolic profiling and apparatus and bioinformatics database)
IT Information systems
(retrieval; polypeptide fingerprinting methods and metabolic profiling and apparatus and bioinformatics database)
IT Disease, animal
(screening for metabolites correlated with; polypeptide fingerprinting methods and metabolic profiling and apparatus and bioinformatics database)
IT Information systems
(searching, protein sequence databases; polypeptide fingerprinting methods and metabolic profiling and apparatus and bioinformatics database)
IT **Proteins, general, analysis**
RL: ANT (Analyte); BOC (Biological occurrence); BSU (Biological study, unclassified); MFM (Metabolic formation); PRP (Properties); ANST (Analytical study); BIOL (Biological study); FORM (Formation, nonpreparative); OCCU (Occurrence)
(separation; polypeptide fingerprinting methods and metabolic profiling and apparatus and bioinformatics database)
IT Albumins, analysis
RL: ANT (Analyte); PEP (Physical, engineering or chemical process); RCT (Reactant); ANST (Analytical study); PROC (Process); RACT (Reactant or reagent)
(serum, bovine, separation of mixture containing; polypeptide fingerprinting methods and metabolic profiling and apparatus and bioinformatics database)
IT Mass
(signature, labeling agent having unique; polypeptide fingerprinting methods and metabolic profiling and apparatus and bioinformatics database)
IT Information systems
(storage; polypeptide fingerprinting methods and metabolic profiling and apparatus and bioinformatics database)
IT Capillary electrophoresis apparatus
Capillary electrophoresis apparatus
(zone; polypeptide fingerprinting methods and metabolic profiling and apparatus and bioinformatics database)
IT 9001-99-4
RL: ANT (Analyte); PEP (Physical, engineering or chemical process); RCT (Reactant); ANST (Analytical study); PROC (Process); RACT (Reactant or reagent)
(A, bovine, separation of mixture containing; polypeptide fingerprinting methods
and metabolic profiling and apparatus and bioinformatics database)
IT 9001-03-0
RL: ANT (Analyte); PEP (Physical, engineering or chemical process); RCT (Reactant); ANST (Analytical study); PROC (Process); RACT (Reactant or reagent)
(II, separation of mixture containing; polypeptide fingerprinting methods and
metabolic profiling and apparatus and bioinformatics database)
IT 50-99-7, Glucose, biological studies 110187-42-3, [13C]6-Glucose
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(detecting metabolites of, in Escherichia coli; polypeptide fingerprinting methods and metabolic profiling and apparatus and bioinformatics database)
IT 65-61-2, Acridine orange 82-76-8 7620-46-4, 9-Isothiocyanatoacridine 7724-15-4 16707-41-8, N-(p-(2-Benzoxazolyl)phenyl)maleimide 51278-31-0 55936-32-8, 3-Phenyl-7-isocyanatocoumarin
RL: ARG (Analytical reagent use); PRP (Properties); RCT (Reactant); ANST (Analytical study); RACT (Reactant or reagent); USES (Uses)
(fluorophore for detection enhancement; polypeptide fingerprinting methods and metabolic profiling and apparatus and bioinformatics database)

IT 220713-84-8, NanoOrange 303030-95-7, Quantum Dye
RL: ARG (Analytical reagent use); RCT (Reactant); ANST (Analytical study); RACT (Reactant or reagent); USES (Uses)
(fluorophore for detection enhancement; polypeptide fingerprinting methods and metabolic profiling and apparatus and bioinformatics database)
IT 91-64-5D, Coumarin, compds. 129-00-0D, Pyrene, compds., reactions
260-94-6D, Acridine, compds. 273-09-6D, 2,1,3-Benzoxadiazole, derivs.
588-59-0D, Stilbene, compds. 25168-10-9D, Naphthylamine, compds.
RL: ARG (Analytical reagent use); PRP (Properties); RCT (Reactant); ANST (Analytical study); RACT (Reactant or reagent); USES (Uses)
(fluorophores, for detection enhancement; polypeptide fingerprinting methods and metabolic profiling and apparatus and bioinformatics database)
IT 9032-10-4D, Glycogen phosphorylase A, acetylated
RL: PRP (Properties)
(inverted mass ladder sequencing of; polypeptide fingerprinting methods and metabolic profiling and apparatus and bioinformatics database)
IT 58-82-2, Bradykinin
RL: PRP (Properties); RCT (Reactant); RACT (Reactant or reagent)
(inverted mass ladder sequencing of; polypeptide fingerprinting methods and metabolic profiling and apparatus and bioinformatics database)
IT 302788-43-8P, PITC-Bradykinin 302788-44-9P, Iminobiotin-bradykinin
302788-45-0P
RL: PRP (Properties); SPN (Synthetic preparation); PREP (Preparation)
(inverted mass ladder sequencing of; polypeptide fingerprinting methods and metabolic profiling and apparatus and bioinformatics database)
IT 103-72-0, Phenylisothiocyanate 3399-67-5, 2-AETA 25952-53-8, EDC
84171-51-7, NHS-iminobiotin
RL: RCT (Reactant); RACT (Reactant or reagent)
(polypeptide fingerprinting methods and metabolic profiling and apparatus and bioinformatics database)
IT 7216-63-9, 4-Sulfophenylisothiocyanate
RL: RCT (Reactant); RACT (Reactant or reagent)
(protein labeling with, protein separation in relation to; polypeptide fingerprinting methods and metabolic profiling and apparatus and bioinformatics database)
IT 302788-42-7, GAPDH
RL: ANT (Analyte); PEP (Physical, engineering or chemical process); RCT (Reactant); ANST (Analytical study); PROC (Process); RACT (Reactant or reagent)
(rabbit muscle, separation of mixture containing; polypeptide fingerprinting methods and metabolic profiling and apparatus and bioinformatics database)
RE.CNT 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE
(1) Aebersold; US 5856082 A 1999 HCAPLUS
(2) Jensen, O; Electrophoresis 1996, V15(5), P938
(3) Karger; US 5872010 A 1999
(4) LI, G; Book of Abstracts, 213th ACS National Meeting 1997
(5) Laukien; US 5505832 A 1996 HCAPLUS
(6) Lee; US 4994165 A 1991 HCAPLUS
(7) Mann, M; Analytical Chemistry 1994, V66(24), P4390 HCAPLUS
(8) Smith; US 4842701 A 1989 HCAPLUS
(9) Whitehouse; US 5306412 A 1994 HCAPLUS
(10) Wilkins, M; Biochemical and Biophysical Research Communications 1996, V221(3), P609 HCAPLUS
(11) Wilkins, M; Current Biology 1996, V6(12), P1543 HCAPLUS
(12) Wilkins, M; J Mol Biol 1998, V278(3), P599 HCAPLUS

L123 ANSWER 12 OF 15 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:592921 HCAPLUS
DN 133:161593

ED Entered STN: 25 Aug 2000
TI Methods for activated eosinophil detection used in the diagnosis of asthma
IN Hazen, Stan; Wu, Weikia; Schmitt, David
PA Cleveland Clinic Foundation, USA
SO PCT Int. Appl., 36 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM G01N033-53
ICS C07C229-00
CC 9-16 (Biochemical Methods)
Section cross-reference(s): 1, 14
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000049411	A1	20000824	WO 2000-US4253	20000218 <--
	RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
	US 6306576	B1	20011023	US 1999-253380	19990219 <--
	EP 1159614	A1	20011205	EP 2000-908730	20000218 <--
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
	US 2002048775	A1	20020425	US 2001-931287	20010816 <--
PRAI	US 1999-253380	A	19990219 <--		
	WO 2000-US4253	W	20000218 <--		

AB Screening methods for asthma and analogous diseases in which activated eosinophils are found at the disease site are provided. The methods involve assaying for the presence of brominated tyrosine species in a bodily sample which has been obtained from a test subject. The brominated tyrosine species are either free in the sample or protein bound. In one embodiment, the assay involve measuring the amount of a brominated tyrosine species, particularly 3-bromotyrosine, 3,5-dibromotyrosine, or combinations thereof (referred to hereinafter collectively as the "diagnostic marker") in a bodily sample from the test subject. In another embodiment for determining the prognosis of asthma in a test subject, the concentration or content of the diagnostic marker is determined in bodily samples taken from the test subject over successive time intervals. The concns. are compared to determine the prognosis of the asthma. In another embodiment of the invention for monitoring the response of the test subject to treatment with an anti-asthmatic drug, the concentration or content of the diagnostic marker is measured in bodily samples obtained from the test subject before and after such treatment. The present invention also relates to a diagnostic kit and to a diagnostic reagent for diagnosing asthma and analogous diseases which are associated with activated eosinophils.

ST asthma diagnosis activated eosinophil tyrosine
IT Lung
(alveolus, bronchoalveolar lavage; methods using activated eosinophil detection for diagnosis of asthma)
IT Lung
(broncho-alveolar lavage; methods using activated eosinophil detection for diagnosis of asthma)
IT **Peptides, analysis**
RL: ANT (Analyte); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(containing bromotyrosine; methods using activated eosinophil detection for diagnosis of asthma)
IT HPLC
(electrochem. detection; methods using activated eosinophil detection for diagnosis of asthma)

IT **Mass spectrometry**
Mass spectrometry
(gas chromatog. combined with; methods using activated eosinophil detection for diagnosis of asthma)
IT NMR spectroscopy
(high-resolution; methods using activated eosinophil detection for diagnosis of asthma)
IT Gas chromatography
Gas chromatography
(mass spectrometry combined with; methods using activated eosinophil detection for diagnosis of asthma)
IT Allergy
Antiasthmatics
Asthma
Blood analysis
Blood plasma
Blood serum
Capillary electrophoresis
Cell
Cerebrospinal fluid
Diagnosis
Eosinophil
Feces
Immunoassay
Pleural fluid
Sputum
Urine
Urine analysis
(methods using activated eosinophil detection for diagnosis of asthma)
IT **Peptides, analysis**
RL: ANT (Analyte); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(methods using activated eosinophil detection for diagnosis of asthma)
IT Steroids, biological studies
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(methods using activated eosinophil detection for diagnosis of asthma)
IT Antibodies
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(monoclonal, anti-bromotyrosine; methods using activated eosinophil detection for diagnosis of asthma)
IT Body fluid
(pericardial fluid; methods using activated eosinophil detection for diagnosis of asthma)
IT 60-18-4, Tyrosine, analysis
RL: ANT (Analyte); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(brominated, protein bound; methods using activated eosinophil detection for diagnosis of asthma)
IT 75139-57-0, Kit
RL: NUU (Other use, unclassified); USES (Uses)
(diagnostic; methods using activated eosinophil detection for diagnosis of asthma)
IT 60-18-4D, Tyrosine, brominated 60-18-4D, L-Tyrosine, oxidation products, analysis 300-38-9, 3,5-Dibromotyrosine 38739-13-8
RL: ANT (Analyte); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(methods using activated eosinophil detection for diagnosis of asthma)
IT **7782-39-0**, 2H, uses **14390-96-6**, Nitrogen, isotope of mass 15, atomic, uses **14762-74-4**, 13C, uses

RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(methods using activated eosinophil detection for diagnosis of asthma)
RE.CNT 1 THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE
(1) Grose; US 5710248 A 1998 HCAPLUS
IT **7782-39-0**, 2H, uses **14390-96-6**, Nitrogen, isotope of mass 15, atomic, uses **14762-74-4**, 13C, uses
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(methods using activated eosinophil detection for diagnosis of asthma)
RN 7782-39-0 HCAPLUS
CN Deuterium (7CI, 8CI, 9CI) (CA INDEX NAME)

D—D

RN 14390-96-6 HCAPLUS
CN Nitrogen, isotope of mass 15, at. (8CI, 9CI) (CA INDEX NAME)

^{15}N

RN 14762-74-4 HCAPLUS
CN Carbon, isotope of mass 13 (8CI, 9CI) (CA INDEX NAME)

^{13}C

L123 ANSWER 13 OF 15 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:111538 HCAPLUS
DN 132:305435
ED Entered STN: 17 Feb 2000
TI Identification and C-Terminal Characterization of Proteins from Two-Dimensional Polyacrylamide Gels by a Combination of Isotopic Labeling and Nanoelectrospray Fourier Transform Ion Cyclotron Resonance Mass Spectrometry
AU Kosaka, Toshiyuki; Takazawa, Tomoko; Nakamura, Takemichi
CS Biomedical Research Laboratories, Sankyo Company Ltd., Shinagawa-ku Tokyo, 140-8710, Japan
SO Analytical Chemistry (**2000**), 72(6), 1179-1185
CODEN: ANCHAM; ISSN: 0003-2700
PB American Chemical Society
DT Journal
LA English
CC 9-16 (Biochemical Methods)
AB We propose a novel method for the identification and C-terminal characterization of proteins separated by two-dimensional PAGE (2D-PAGE). Proteins were digested in a gel in a buffer solution containing 50% 18O-labeled water, and mixts. of 18O/16O-labeled peptides were analyzed by nanoelectrospray Fourier transform ion cyclotron resonance mass spectrometry (FT-ICR MS). This method was evaluated using horse skeletal muscle myoglobin as the model protein in SDS gel. The high resolution of FT-ICR MS minimized the overlapping of peptide peaks and facilitated identification of the C-terminal peptide, which was done by observing the undisrupted isotope peak pattern. As well, with its low ppm-level high mass accuracy, it can rapidly and reliably identify the in-gel-separated protein and determine its C-terminal by peptide mass fingerprinting alone.

Therefore, this method should be applicable to routine and high-throughput proteome studies. Here, the method was applied to the anal. of rat liver proteins separated by 2D-PAGE. The C-termini of eight proteins were successfully identified out of 10 randomly picked Coomassie brilliant blue-stained spots. The feasibility and limitations of this approach are reported in this paper.

ST characterization protein polyacrylamide gel isotopic labeling; nanoelectrospray Fourier transform ion cyclotron resonance mass spectrometry

IT **Ion cyclotron resonance mass spectrometry**
(Fourier transform, nanoelectrospray; identification and C-terminal characterization of proteins from two-dimensional polyacrylamide gels by a combination of isotopic labeling and nanoelectrospray Fourier transform ion cyclotron resonance mass spectrometry)

IT **Isotope indicators**
Liver
(identification and C-terminal characterization of proteins from two-dimensional polyacrylamide gels by a combination of isotopic labeling and nanoelectrospray Fourier transform ion cyclotron resonance mass spectrometry)

IT Myoglobins
Proteins, general, analysis
RL: ANT (Analyte); PRP (Properties); ANST (Analytical study)
(identification and C-terminal characterization of proteins from two-dimensional polyacrylamide gels by a combination of isotopic labeling and nanoelectrospray Fourier transform ion cyclotron resonance mass spectrometry)

IT **Polyacrylamide gel electrophoresis**
(two-dimensional; identification and C-terminal characterization of proteins from two-dimensional polyacrylamide gels by a combination of isotopic labeling and nanoelectrospray Fourier transform ion cyclotron resonance mass spectrometry)

IT 14314-42-2, Water, labeled with oxygen 18 74434-20-1, Coomassie brilliant blue
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(identification and C-terminal characterization of proteins from two-dimensional polyacrylamide gels by a combination of isotopic labeling and nanoelectrospray Fourier transform ion cyclotron resonance mass spectrometry)

RE.CNT 19 THERE ARE 19 CITED REFERENCES AVAILABLE FOR THIS RECORD

RE

(1) Andersen, H; Electrophoresis 1997, V18, P2091 HCAPLUS
(2) Anderson, N; Electrophoresis 1996, V17, P443 HCAPLUS
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(11) Patterson, D; Anal Chem 1995, V67, P3971 HCAPLUS
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(19) Wilm, M; Anal Chem 1996, V66, P1

L123 ANSWER 14 OF 15 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1999:790684 HCAPLUS
DN 132:163095
ED Entered STN: 15 Dec 1999
TI Proteome analysis using selective incorporation of isotopically labeled amino acids
AU Veenstra, T. D.; Martinovic, S.; Anderson, G. A.; Pasa-Tolic, L.; Smith, R. D.
CS Environmental and Molecular Sciences Laboratory, Pacific Northwest National Laboratories, Richland, WA, USA
SO Journal of the American Society for Mass Spectrometry (2000), 11(1), 78-82
CODEN: JAMSEF; ISSN: 1044-0305
PB Elsevier Science Inc.
DT Journal
LA English
CC 9-16 (Biochemical Methods)
AB A method is described for identifying intact proteins from genomic databases using a combination of accurate mol. mass measurements and partial amino acid content. An initial demonstration was conducted for proteins isolated from Escherichia coli (E. coli) using a multiple auxotrophic strain of K12. Proteins extracted from the organism grown in natural isotopic abundance minimal medium and also minimal medium containing isotopically labeled leucine (Leu-D10), were mixed and analyzed by capillary isoelec. focusing (CIEF) coupled with Fourier transform ion cyclotron resonance mass spectrometry (FTICR). The incorporation of the isotopically labeled Leu residue has no effect on the CIEF separation of the protein, therefore both versions of the protein are observed within the same FTICR spectrum. The difference in the mol. mass of the natural isotopic abundance and Leu-D10 isotopically labeled proteins is used to determine the number of Leu residues present in that particular protein. Knowledge of the mol. mass and number of Leu residues present can be used to unambiguously identify the intact protein. Preliminary results show the efficacy of this method for unambiguously identifying proteins isolated from E. coli.
ST proteome analysis selective incorporation amino acid isotope labeled; protein detn mass spectrometry capillary isoelec focusing
IT **Ion cyclotron resonance mass spectrometry**
(Fourier transform; proteome anal. using selective incorporation of isotopically labeled amino acids)
IT Culture media
(Leu-D10 containing; proteome anal. using selective incorporation of isotopically labeled amino acids)
IT **Proteins, general, analysis**
RL: ANT (Analyte); BPN (Biosynthetic preparation); ANST (Analytical study); BIOL (Biological study); PREP (Preparation)
(exts. from E.coli; proteome anal. using selective incorporation of isotopically labeled amino acids)
IT **Capillary isoelectric focusing**
Escherichia coli
(proteome anal. using selective incorporation of isotopically labeled amino acids)
IT **Isotopes**
RL: ANT (Analyte); ANST (Analytical study)
(proteome anal. using selective incorporation of isotopically labeled amino acids)
IT Amino acids, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)

(proteome anal. using selective incorporation of isotopically labeled amino acids)
IT 106972-44-5
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(proteome anal. using selective incorporation of isotopically labeled amino acids)
RE.CNT 19 THERE ARE 19 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE
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L123 ANSWER 15 OF 15 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1997:422738 HCAPLUS
DN 127:146619
ED Entered STN: 09 Jul 1997
TI Rapid 'de Novo' **peptide** sequencing by a combination of nanoelectrospray, **isotopic labeling** and a quadrupole/time-of-flight mass spectrometer
AU Shevchenko, Andrej; Chernushevich, Igor; Ens, Werner; Standing, Kenneth G.; Thomson, Bruce; Wilm, Matthias; Mann, Matthias
CS Protein & Peptide Group, European Molecular Biology Lab. (EMBL), Heidelberg, D-69117, Germany
SO Rapid Communications in Mass Spectrometry (**1997**), 11(9), 1015-1024
CODEN: RCMSEF; ISSN: 0951-4198
PB Wiley
DT Journal
LA English
CC 9-5 (Biochemical Methods)
AB Protein microanal. usually involves the sequencing of gel-separated proteins available in very small amts. While mass spectrometry has become the method of choice for identifying proteins in databases, in almost all labs. 'de novo' protein sequencing is still performed by Edman degradation Here we show that a combination of the nanoelectrospray ion source, isotopic end labeling of peptides and a quadrupole/time-of-flight instrument allows facile read-out of the sequences of tryptic peptides. Isotopic labeling was performed by enzymic digestion of proteins in 1:1 16O/18O water, eliminating the need for peptide derivatization. A quadrupole/time-of-flight mass spectrometer was constructed from a triple quadrupole and an electrospray time-of-flight instrument. Tandem mass spectra of peptides were obtained with better than 50 ppm mass accuracy and resolution routinely in excess of 5000. Unique and error tolerant

identification of yeast proteins as well as the sequencing of a novel protein illustrate the potential of the approach. The high data quality in tandem mass spectra and the addnl. information provided by the isotopic end labeling of peptides enabled automated interpretation of the spectra via simple software algorithms. The technique demonstrated here removes one of the last obstacles to routine and high throughput protein sequencing by mass spectrometry.

ST **peptide** sequencing nanoelectrospray **isotopic labeling**; quadrupole time flight mass spectrometer

IT Mass spectrometry
(quadrupole/time-of-flight; rapid 'de Novo' **peptide** sequencing by a combination of nanoelectrospray, **isotopic labeling** and a quadrupole/time-of-flight mass spectrometer)

IT Algorithm
Protein sequence analysis
(rapid 'de Novo' **peptide** sequencing by a combination of nanoelectrospray, **isotopic labeling** and a quadrupole/time-of-flight mass spectrometer)

IT **Peptides, analysis**
RL: ANT (Analyte); ANST (Analytical study)
(rapid 'de Novo' **peptide** sequencing by a combination of nanoelectrospray, **isotopic labeling** and a quadrupole/**time**-of-**flight mass spectrometer**)

=> d his

(FILE 'HOME' ENTERED AT 07:08:12 ON 11 MAR 2004)

FILE 'REGISTRY' ENTERED AT 07:08:21 ON 11 MAR 2004

```
                E C/MF
L1             62 S E3
L2             41 S L1 AND ISOTOPE
                E N/MF
L3             28 S E3 AND ISOTOPE
                E H/MF
L4              7 S E3 AND ISOTOPE
                E D/MF
L5              4 S E3
                E T/MF
L6              3 S E3
                E  C5H8D3NO2S/MF
L7             11 S E3
                E  C5H8T3NO2S/MF
                E C9H18O5S/MF
L8             66 S E3
L9             20 S L8 AND OC5/ES
L10            11 S L9 AND (GLUCOPYRANOSIDE OR GALACTOPYRANOSIDE)
L11             8 S L10 AND (METHYLETHYL OR PROPYL)
L12             2 L11 AND ALPHA
L13             1 S L12 NOT METHYLETHYL
L14             6 S L11 NOT L12
L15             7 S L14 OR L13
                E C2H3D2NO2/MF
L16             8 S E3
L17             5 S L16 AND GLYCINE
L18             2 S 9002-07-7 OR 9001-92-7
L19             9 S L7 AND METHIONINE
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     FILE 'HCAPLUS' ENTERED AT 07:53:41 ON 11 MAR 2004
L20       65191 MASS SPECTROMETRY+OLD,NT/CT
L21       12631 MASS SPECTROMETERS+OLD,NT/CT
L22       38654 MASS SPECTRA+NT/CT
L23        9004 ISOTOPE SEPARATION+NT/CT
L24      388835 ISOTOPES+NT/CT
L25      707102 S PROTEINS+OLD/CT
L26      514363 E2-7/CC,SX
L27       15964 S L25 (L) (IDENTIF? OR TAG? OR ?MARK?/BI)
L28       14799 S L25 (L) (SEPARAT? OR ISOLAT? OR SECLU!?)
L29         422 S L25 (L) (?RADIOLABEL?/BI OR (?RADIO?/BI () LABEL?) OR ?ISOTOP
L30        9284 GEL ELECTROPHORESIS+NT/CT
L31        9608 S L25 (L) PUR/RL
L32      145550 S MASS SPECTR!?
L33       18508 GEL ELECTROPHOR?
L34        2149 S (MALDI OR MATRIX ASSISTED LASER DESORPTION IONIZAT?) (L) (TOF
L35        2064 S (MALDI OR MATRIX ASSISTED LASER DESORPTION IONIZAT?) (L) (TOF
L36        8047 S (TOF OR TIME OF FLIGHT) (L) (MS OR L32)
L37        7071 PEPTIDES, ANALYSIS/CT
L38       16118 S (?PROTEIN?/BI OR AMINO ACID? OR ?PEPTID?/BI) (L) (?RADIOLABEL
L39      198562 S (?PROTEIN?/BI OR AMINO ACID? OR ?PEPTID?/BI) (L) (IDENTIF? OR
L40      247504 S (?PROTEIN?/BI OR AMINO ACID? OR ?PEPTID?/BI) (L) (SEPARAT? OR
L41        1226 S (L32 OR L34-36) (L) L37
L42          16 S L41 AND L38
L43           4 S L42 AND (PRD<20010112 OR AD<20010112 OR PD<20010112)
L44       44659 ELECTROPHORESIS+OLD,NT/CT
L45         238 S L20-22 AND L27 AND (L28 OR L33 OR L44)
L46          10 S L45 AND L24
L47           4 S L46 AND (PRD<20010112 OR AD<20010112 OR PD<20010112)
L48           8 S L43 OR L47
L49        6759 ISOTOPE INDICATORS/CT
L50      124247 S PEPTIDE#/CW
L51      993544 PROTEIN#/CW
L52           9 MS/CW
L53         111 MALDI (L) TOFMS
L54        2384 S PROTEOME/CT
L55        2384 S PROTEOME#/CW
L56       55129 L2-6

     FILE 'REGISTRY' ENTERED AT 10:18:58 ON 11 MAR 2004
L57          83 S L2-6

     FILE 'HCAPLUS' ENTERED AT 10:36:28 ON 11 MAR 2004
L58          52 S L20-22 AND (L23-24 OR L49 OR L57) AND (L25 OR L37 OR L50-51 O
L59          25 S L58 AND (PRD<20010112 OR AD<20010112 OR PD<20010112)
L60          52 S L20-22 AND (L23-24 OR L49 OR L56) AND (L25 OR L37 OR L50-51 O
L61          25 S L60 AND (PRD<20010112 OR AD<20010112 OR PD<20010112)
L62          25 S L59 OR L61
L63       12121 S (L25 OR L37 OR L50-51 OR L54-55) (L) PUR/RL
L64       52900 S (L25 OR L37 OR L50-51 OR L54-55) (L) ANST+NT/RL
L65       26789 S (L25 OR L37 OR L50-51 OR L54-55) (L) (ISOLAT? OR PURIF?)
L66         308 S L20-22 AND (L23-24 OR L49 OR L56) AND (L25 OR L37 OR L50-51 O
L67         146 S L66 AND (PRD<20010112 OR AD<20010112 OR PD<20010112)
L68          16 S L59 NOT (1990:420539 OR 1998:477959 OR 1999:764230 OR 2001:78
L69       58164 S L17-19
L70           4 S L68 AND L69
L71          12 S L68 NOT L70

     FILE 'HCAPLUS' ENTERED AT 11:49:31 ON 11 MAR 2004
               ACT GIT965/A
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L72  (         62)SEA FILE=REGISTRY ABB=ON  PLU=ON  C/MF
L73  (         21)SEA FILE=REGISTRY ABB=ON  PLU=ON  L72 NOT ISOTOPE
L74  (         41)SEA FILE=REGISTRY ABB=ON  PLU=ON  L72 NOT L73
L75  (         40)SEA FILE=REGISTRY ABB=ON  PLU=ON  N/MF
L76  (         28)SEA FILE=REGISTRY ABB=ON  PLU=ON  L75 AND ISOTOPE
L77  (         21)SEA FILE=REGISTRY ABB=ON  PLU=ON  H/MF
L78  (          7)SEA FILE=REGISTRY ABB=ON  PLU=ON  L77 AND ISOTOPE
L79(           4)SEA FILE=REGISTRY ABB=ON  PLU=ON  D/MF
L80(           3)SEA FILE=REGISTRY ABB=ON  PLU=ON  T/MF
L81(          83)SEA FILE=REGISTRY ABB=ON  PLU=ON  L74 OR L76 OR (L78 OR L79 OR
L82(       38651)SEA FILE=HCAPLUS ABB=ON  PLU=ON  MASS SPECTRA+NT/CT
L83(       10767)SEA FILE=HCAPLUS ABB=ON  PLU=ON  MASS SPECTROMETERS+OLD/CT
L84(         727)SEA FILE=HCAPLUS ABB=ON  PLU=ON  TIME-OF-FLIGHT MASS SPECTROMET
L85(         790)SEA FILE=HCAPLUS ABB=ON  PLU=ON  L83 (L) TIME OF FLIGHT/OBI
L86(       21938)SEA FILE=HCAPLUS ABB=ON  PLU=ON  MASS SPECTROSCOPY/CT
L87(       29515)SEA FILE=HCAPLUS ABB=ON  PLU=ON  MASS SPECTROMETRY/CT
L88(        1067)SEA FILE=HCAPLUS ABB=ON  PLU=ON  (L86 OR L87) (L) TIME OF FLI
L89(        3160)SEA FILE=HCAPLUS ABB=ON  PLU=ON  TIME-OF-FLIGHT MASS SPECTROMET
L90(         153)SEA FILE=HCAPLUS ABB=ON  PLU=ON  (L86 OR L87) (L) (PHOTODESOR
L91(        3738)SEA FILE=HCAPLUS ABB=ON  PLU=ON  LASER DESORPTION MASS SPECTROM
L92(        3369)SEA FILE=HCAPLUS ABB=ON  PLU=ON  L91 (L) PHOTOIONIZATION, MATR
L93(        1131)SEA FILE=HCAPLUS ABB=ON  PLU=ON  (ISOTOP?/OBI (W) (LABEL?/OBI O
L94(       43158)SEA FILE=HCAPLUS ABB=ON  PLU=ON  (PROTEIN?/OBI OR AMINO ACID?/O
L95(       44685)SEA FILE=HCAPLUS ABB=ON  PLU=ON  (PROTEIN?/OBI OR AMINO ACID?/O
L96(        8042)SEA FILE=HCAPLUS ABB=ON  PLU=ON  (TOF/OBI OR TIME OF FLIGHT/OBI
L97(        3895)SEA FILE=HCAPLUS ABB=ON  PLU=ON  (MALDI/OBI OR MATRIX ASSISTED
L98(        2062)SEA FILE=HCAPLUS ABB=ON  PLU=ON  (MALDI/OBI OR MATRIX ASSISTED
L99(         526)SEA FILE=HCAPLUS ABB=ON  PLU=ON  MALDI/OBI (W) (TOF MS/OBI OR T
L100(        502)SEA FILE=HCAPLUS ABB=ON  PLU=ON  (L82 OR L83 OR L84 OR L85
L101(         76)SEA FILE=HCAPLUS ABB=ON  PLU=ON  L100 AND L95
L102(         60)SEA FILE=HCAPLUS ABB=ON  PLU=ON  L101 AND (PRD<20010112 OR AD<2
L103(      55119)SEA FILE=HCAPLUS ABB=ON  PLU=ON  L81
L104(          1)SEA FILE=HCAPLUS ABB=ON  PLU=ON  L103 AND L102
L105(         88)SEA FILE=HCAPLUS ABB=ON  PLU=ON  L103 AND L93 AND (L93 OR L11
L106(      18507)SEA FILE=HCAPLUS ABB=ON  PLU=ON  GEL ELECTROPHOR?/OBI
L107(         15)SEA FILE=HCAPLUS ABB=ON  PLU=ON  (L95 OR L106) AND L105
L108(          4)SEA FILE=HCAPLUS ABB=ON  PLU=ON  L107 AND (STABLE ISOTOPE LABEL
L109(       1265)SEA FILE=HCAPLUS ABB=ON  PLU=ON  (ISOTOP?/OBI (W) (LABEL?/OBI O
L110(        169)SEA FILE=HCAPLUS ABB=ON  PLU=ON  (L95 OR L109) AND (L93 OR L1
L111(        108)SEA FILE=HCAPLUS ABB=ON  PLU=ON  L110 AND (PRD<20010112 OR AD<2
L112(          6)SEA FILE=HCAPLUS ABB=ON  PLU=ON  L111 AND L103
L113(          3)SEA FILE=HCAPLUS ABB=ON  PLU=ON  L112 NOT (1997:256565 OR 1993:
L114(          6)SEA FILE=HCAPLUS ABB=ON  PLU=ON  L104 OR L108 OR L113
L115(          5)SEA FILE=HCAPLUS ABB=ON  PLU=ON  L114 NOT (CLONING, PURIFICATIO
L116(         52)SEA FILE=HCAPLUS ABB=ON  PLU=ON  (L95 OR L109) AND (L93 OR L1
L117(          5)SEA FILE=HCAPLUS ABB=ON  PLU=ON  L116 AND L103
L118           7 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L115 OR L117
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L119          24 S L68 OR L118 OR L48
L120           8 S L119 AND L69
L121          16 S L119 NOT L120
L122           5 S L120 AND (PRD<20010112 OR AD<20010112 OR PD<20010112)
L123          15 S L121 AND (PRD<20010112 OR AD<20010112 OR PD<20010112)

=> b home
FILE 'HOME' ENTERED AT 12:21:01 ON 11 MAR 2004

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